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# FIG. 1

<i>Bet v 1</i> sense	5' - AATTATGAGACTGAGACC <u>A</u> CCTCTGTTATCCCAGCAGCTCG	-3'
<i>Bet v 1</i> non-sense	3' - TTAATACTCTGACTCTGG <u>I</u> GGAGACAATAGGGTCGTCGAGC	-5'
sense primer	5' - TGAGACCC <u>C</u> CCTCTGTTATCCCAG	-3'
non-sense primer	3' - ATACTCTGACTCTGG <u>G</u> GGAGACA	-5'

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## FIG. 2

all	sense	1: 183Bv, 15-mer 5'-GTTGCCAACGATCAG
1	sense	2: 184Bv, 23-mer 5'-TGAGACCCCCTCTGTTATCCCAG
1	non-sense	3: 185Bv, 23-mer 5'-ACAGAGGGGGTCTCAGTCTCATA
2	sense	4: 186Bv, 31-mer 5'-GATACCCCTCTTTCCACAGGTTGCACCCCAAG
2	non-sense	5: 187Bv, 31-mer 5'-ACCTGTGGAAAGAGGGTATCGCCATCAAGGA
3	sense	6: 188Bv, 23-mer 5'-AACATTTTCAGGAAATGGAGGGCC
3	non-sense	7: 189Bv, 23-mer 5'-TTTCCTGAAATGTTTTCAACACT
4	sense	8: 190Bv, 23-mer 5'-TTAAGAACATCAGCTTTCCCGAA
4	non-sense	9: 191Bv, 23-mer 5'-AGCTGATGTTCTTAATGGTTCCA
5	sense	10: 192Bv, 23-mer 5'-GGACCATGCAAAC TTCAAATACA
5	non-sense	11: 193Bv, 23-mer 5'-AGTTTGCATGGTCCACCTCATCA
6	sense	12: 194Bv, 23-mer 5'-TTTCCCTCAGGCCTCCCTTTCAA
6	non-sense	13: 195Bv, 23-mer 5'-AGGCCTGAGGGAAAGCTGATCTT
7	sense	14: 196Bv, 24-mer 5'-TGAAGGATCTGGAGGGCCTGGAAC
7	non-sense	15: 197Bv, 24-mer 5'-CCCTCCAGATCCTTCAATGTTTTC
8	sense	16: 198Bv, 24-mer 5'-GGCAACTGGTGATGGAGGATCCAT
8	non-sense	17: 199Bv, 24-mer 5'-CCATCACCAGTTGCCACTATCTTT
all	non-sense	18: 200Bv, 15-mer 5'-CATGCCATCCGTAAG

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# FIG. 3

1 (A-C)

GGTGTGTTTAAATTATGAGACTGAGACCACTCTGTTATCCCAGCAGCTCGACTGTTCAAG 60  
 G V F N Y E T E T T - P S V I P A A R L F K 20

9 (A-G) 2 (A-C) 2 (A-C)

GCCTTTATCCTTGATGGCGATAACCTCTTTCCAAGGTTGCACCCCAAGCCATTAGCAGT 120  
 A F I L D - G G D N - T L F P K - Q V A P Q A I S S 40

3 (GA-TC) 7 (AA-TC) 4 (G-C) 6 (GA-TC)

GTTGAAAACATTGAAGGAAATGGAGGGCCTGGAACCATTAAGAAATCAGCTTTCCCGAA 180  
 V E N I E - S G N - S G G P G T I K K - N I S F P E - S 60

5 (CA-TG)

GGCCTCCCTTTCAAGTACGTGAAGGACAGAGTTGATGAGGTGGACCACAAACTTCAAA 240  
 G L P F K Y V K D R V D E V D H T - A N F K 80

TACAATTACAGCGTGATCGAGGGCGGTCCCATAGGCGACACATTGGAGAAGATCTCCAAC 300  
 Y N Y S V I E G G P I G D T L E K I S N 100

10 (GAG-CAC) 8 (CCC-TGG)

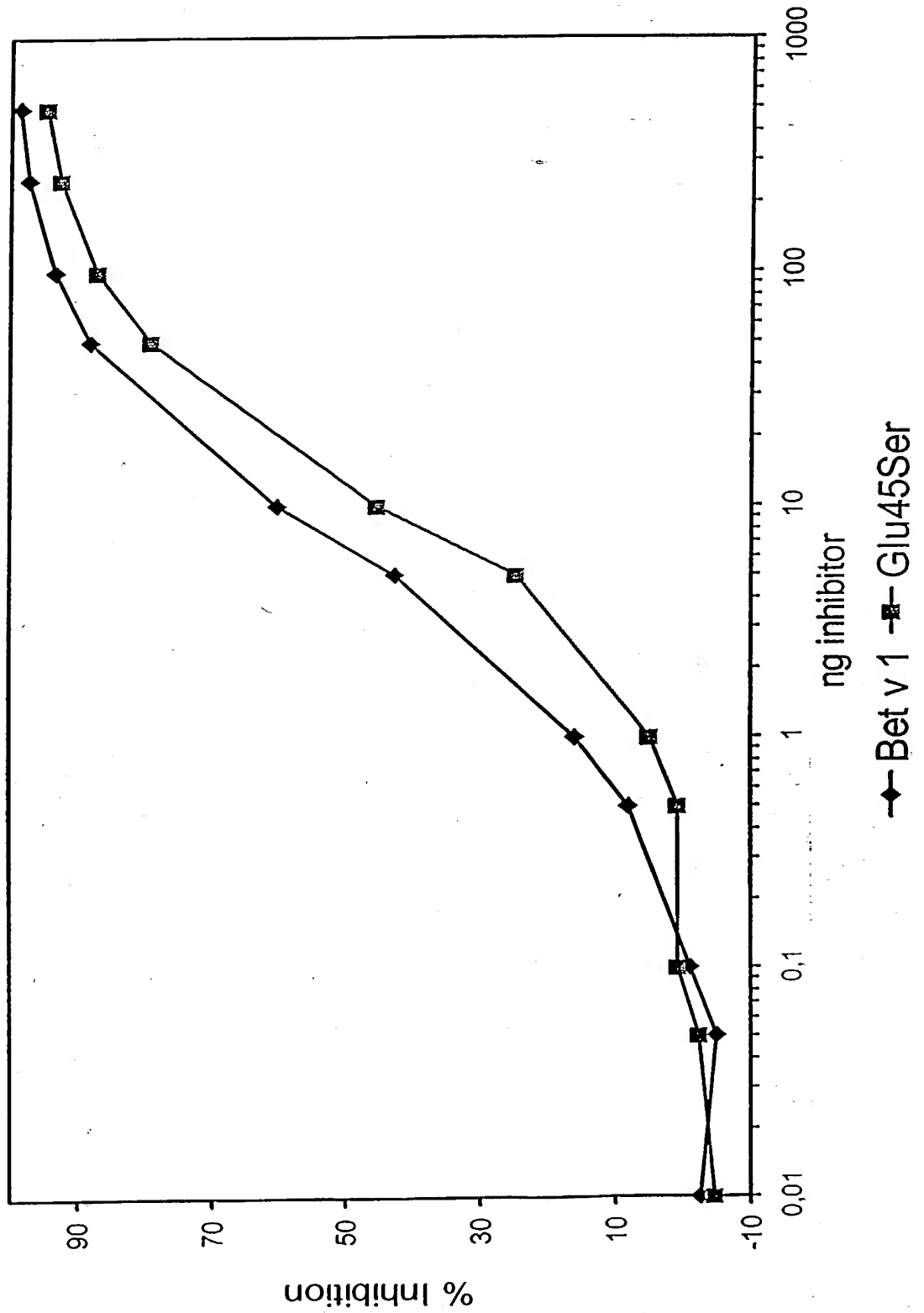
GAGATAAAGATAGTGGCAACCCCTGATGGAGGATCCATCTTGAAGATCAGCAACAAGTAC 360  
 E I K I V A T P - G D G G S I L K I S N K Y 120

CACACCAAAGGTGACCATGAGGTGAAGGCAGAGCAGGTTAAGGCAAGTAAAGAAATGGGC 420  
 H T K G D H E V K A E Q V K A S K E M G 140

GAGACACTTTTGAGGGCCGTTGAGAGCTACCTCTTGGCACACTCCGATGCCTACAATAA 480  
 E T L L R A V E S Y L L A H S D A Y N stop 159



FIG. 4

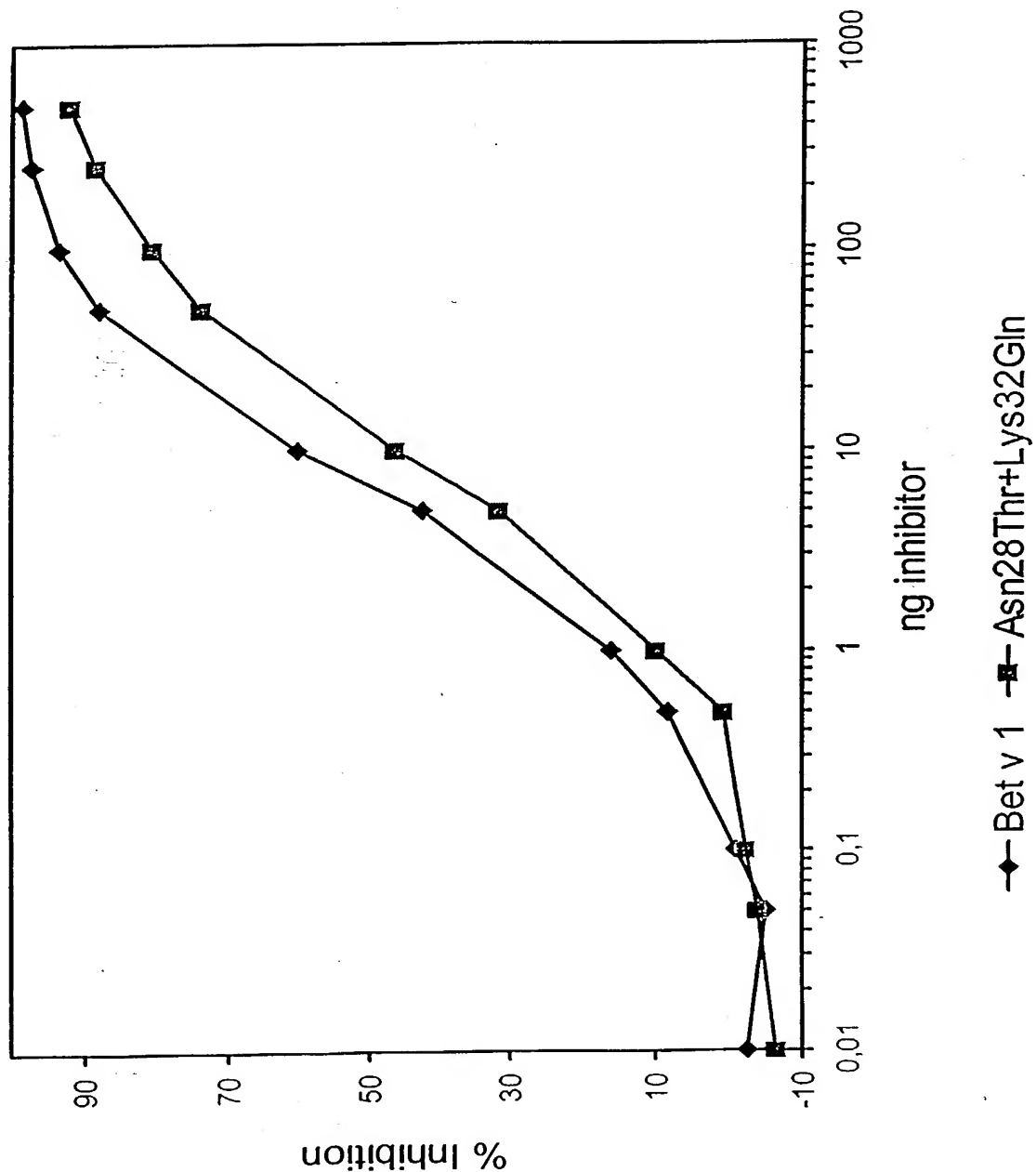




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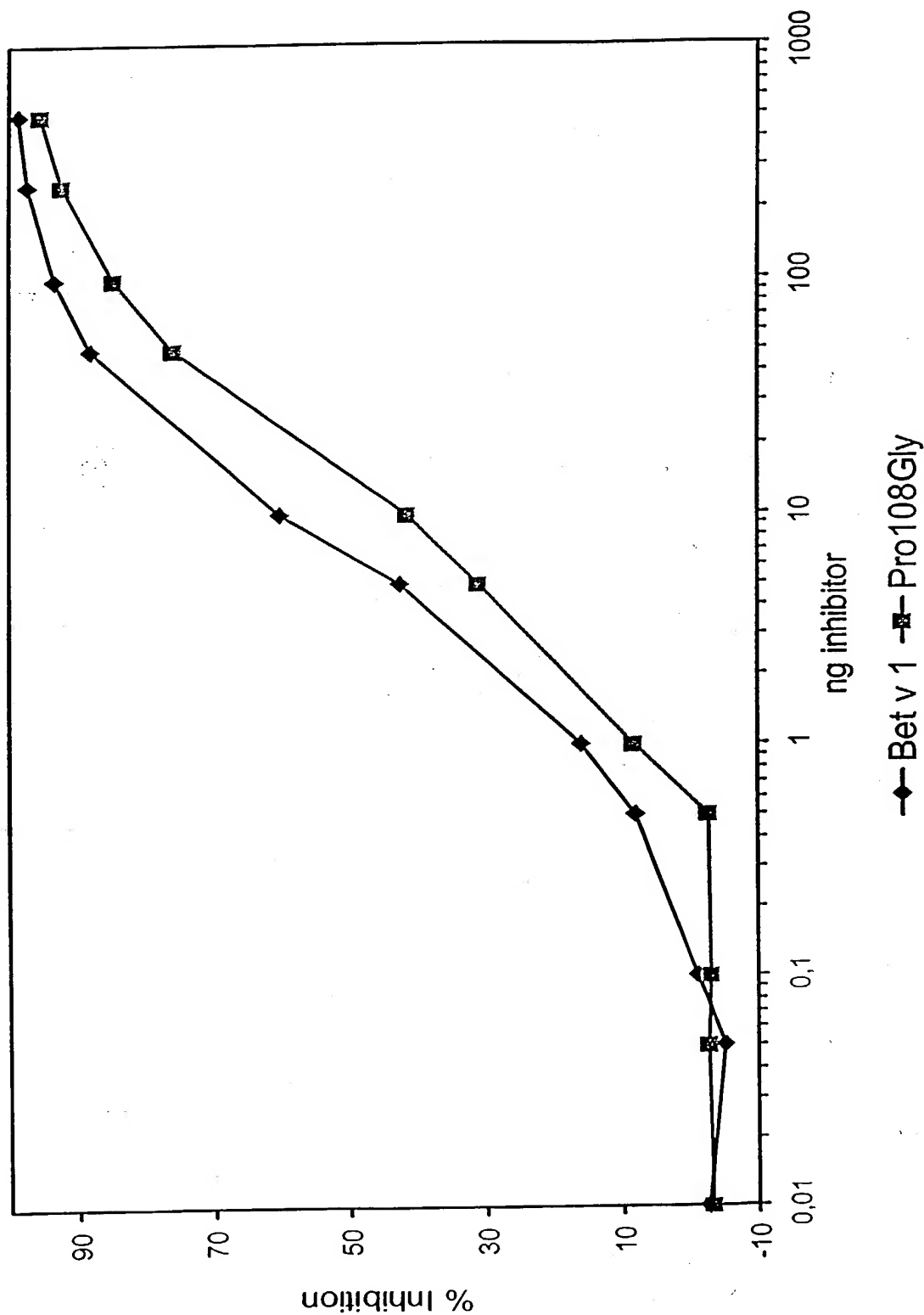
FIG. 5



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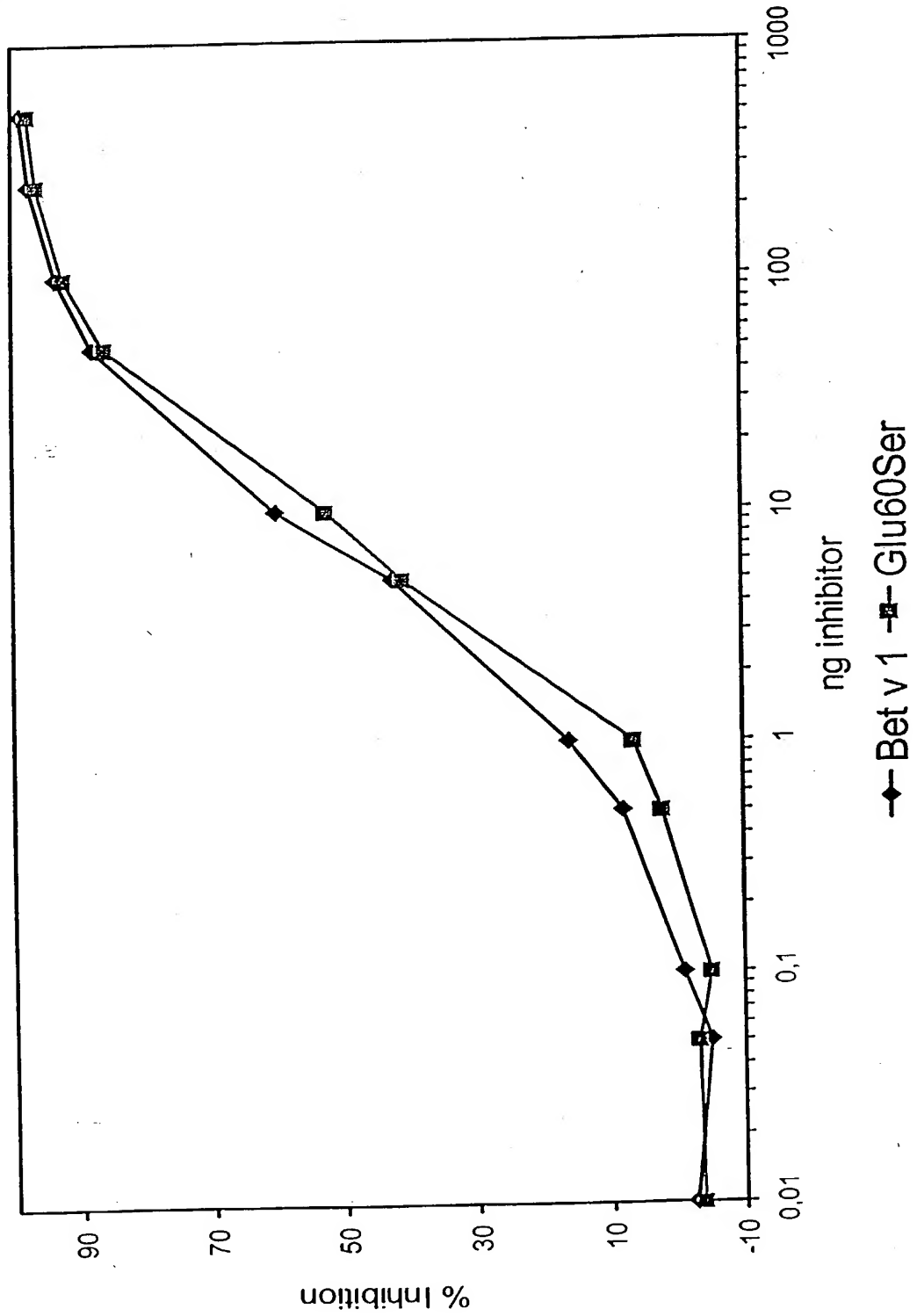
FIG. 6



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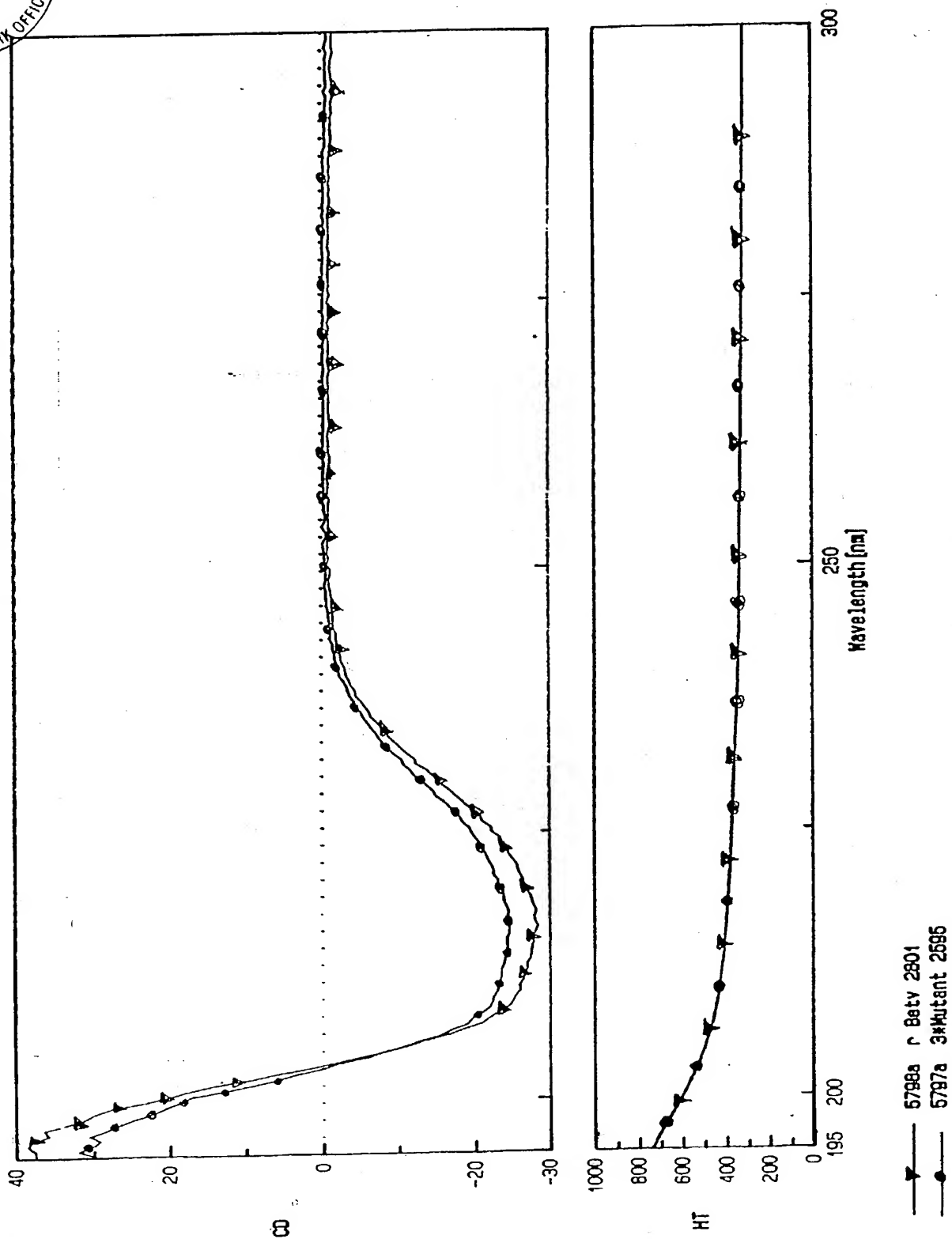
FIG. 7



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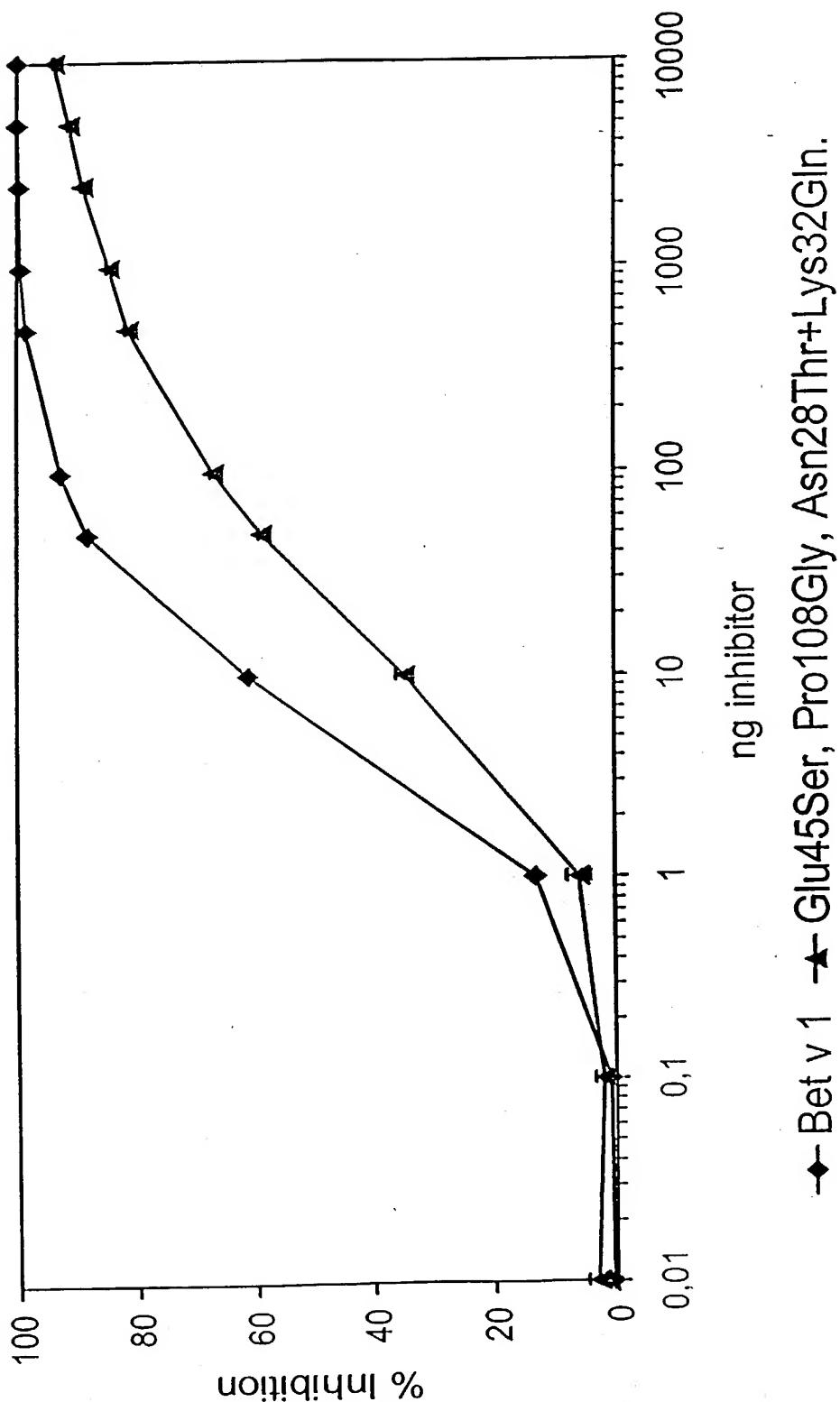
FIG. 8



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FIG. 9



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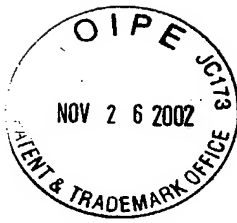
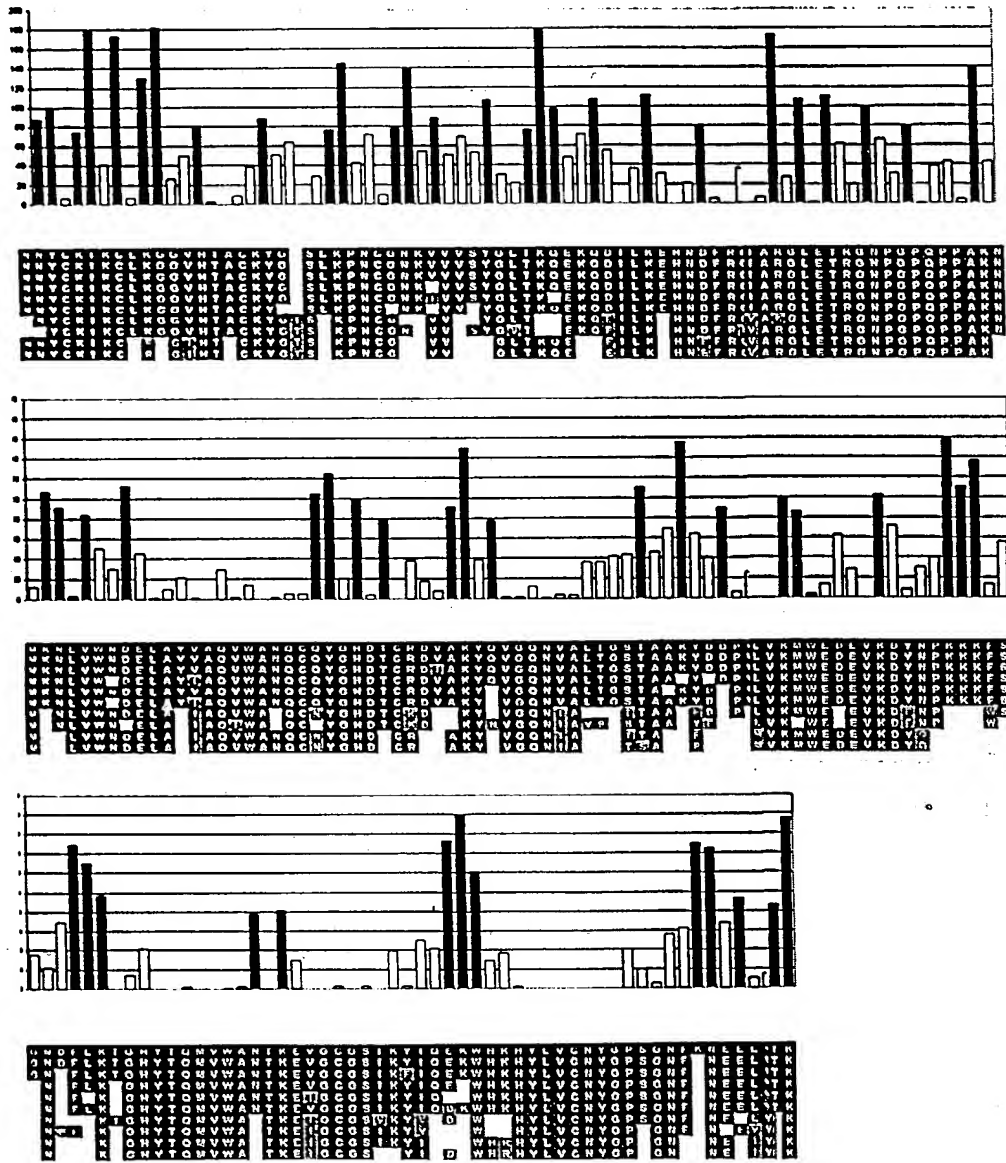


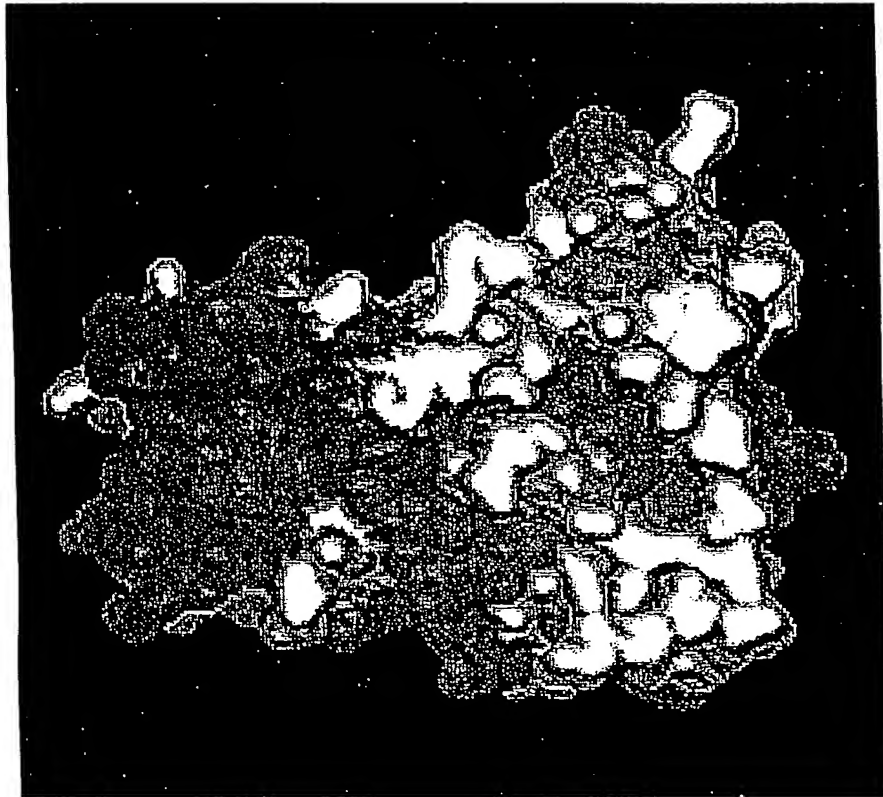
FIG. 10 A



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**FIG. 10 B**



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## FIG. 11 A

Ves v 5 mutant 1 (K72A)

Ves v 5 sense	5'-	ACCACAGCCTCCAGCGAAGAATATGAAAAATTTGGTATGGA	-3'
Ves v 5 non-sense	3'-	TGGTGTCTGGAGGTCGCTTCTTATACTTTTAAACCATACCT	-5'
sense primer	5'-	CCAGCGGCTAATATGAAAAAT	-3'
non-sense primer	3'-	GTCGGAGGTCGCCGATTATAC	-5'

## FIG. 11 B

Ves v 5 mutant 2 (Y96A)

Ves v 5 sense	5'-	GGCTAATCAATGTCAATATGGTCACGATACTTGCAGGGATG	-3'
Ves v 5 non-sense	3'-	CCGATTAGTTACAGTTATACCAGTGCTATGAACGTCCCTAC	-5'
sense primer	5'-	TGTCAAGCTGGTCACGATACT	-3'
non-sense primer	3'-	TTAGTTACAGTTCCGACCAGTG	-5'

## FIG. 12

all sense 1: XhoI start, 38-mer:

EcoRI  
 5'-CCGCTCGAGAAAAGAAACAATTATTGTAAAAATAAAATG  
  L  E  K  R  N  N  Y  C  K  I  K    
 Kex2 cleavage site      amino terminus of Ves v 5

1	sense	1: K72As	21-mer	5'-CCAGCGGCTAATATGAAAAAT
1	non-sense	2: K72Aa	21-mer	5'-CATATTAGCCGCTGGAGGCTG
2	sense	3: Y96As	21-mer	5'-TGTCAAGCTGGTCACGATACT
2	non-sense	4: Y96Aa	21-mer	5'-GTGACCAGCTTGACATGATT
all non-sense 7: CT-pPICZαA, 21-mer				5'-ATTCATCAGCTGCGAGATAGG



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## FIG. 13

1	AACAATTATTGTAAAAATAAAATGTTTGAAAGGAGGTGTCCATACTGCCTGCAAATATGGA	60
1	N N Y C K I K C L K G <u>G</u> V H T A C K Y G	20
61	AGTCTTAAACCGAATTGCGGTAATAAGGTAGTGGTATCCTATGGTCTAACGAAACAAGAG	120
21	S L K P N C G N K V V V S Y G L T K Q E	40
121	AAACAAGACATCTTAAAGGAGCACAATGACTTTAGACAAAAAATTGCACGAGGATTGGAG	180
41	K Q D I L K E H N D F R Q K I A R G L E	60
	1 [K72A] (AAG-GCT)	
181	ACTAGAGGTAATCCTGGACCACAGCCTCCAGCGAAGAATATGAAAAATTTGGTATGGAAC	240
61	T R G N P G P Q P P A K N M K N L V W N	80
	2 [Y96A] (TA-GC)	
241	GACGAGTTAGCTTATGTGCGCCCAAGTGTGGGCTAATCAATGTCAATATGGTCACGATACT	300
81	D E L A Y V A Q V W A N Q C Q Y G H D T	100
301	TGCAGGGATGTAGCAAAATATCAGGTTGGACAAAACGTAGCCTTAACAGGTAGCACGGCT	360
101	C R D V A K Y Q V G Q N V A L T G S T A	120
361	GCTAAATACGATGATCCAGTTAAACTAGTTAAAATGTGGGAAGATGAAGTGAAAGATTAT	420
121	A K Y D D P V K L V K M W E D E V K D Y	140
421	AATCCTAAGAAAAAGTTTTCGGGAAACGACTTTCTGAAAACCGGCCATTACACTCAAATG	480
141	N P K K K F S G N D F L K T G H Y T Q M	160
481	GTTTGGGCTAACACCAAGGAAGTTGGTTGTGGAAGTATAAAATACATTCAAGAGAAATGG	540
161	V W A N T K E V G C G S I K Y I Q E K W	180
541	CACAAACATTACCTTGTATGTAATTATGGACCCAGCGGAAACTTTAAGAATGAGGAACTT	600
181	H K H Y L V C N Y G P S G N F K N E E L	200
601	TATCAAAACAAAGTAA	612
201	Y Q T K stop	204

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FIG. 14

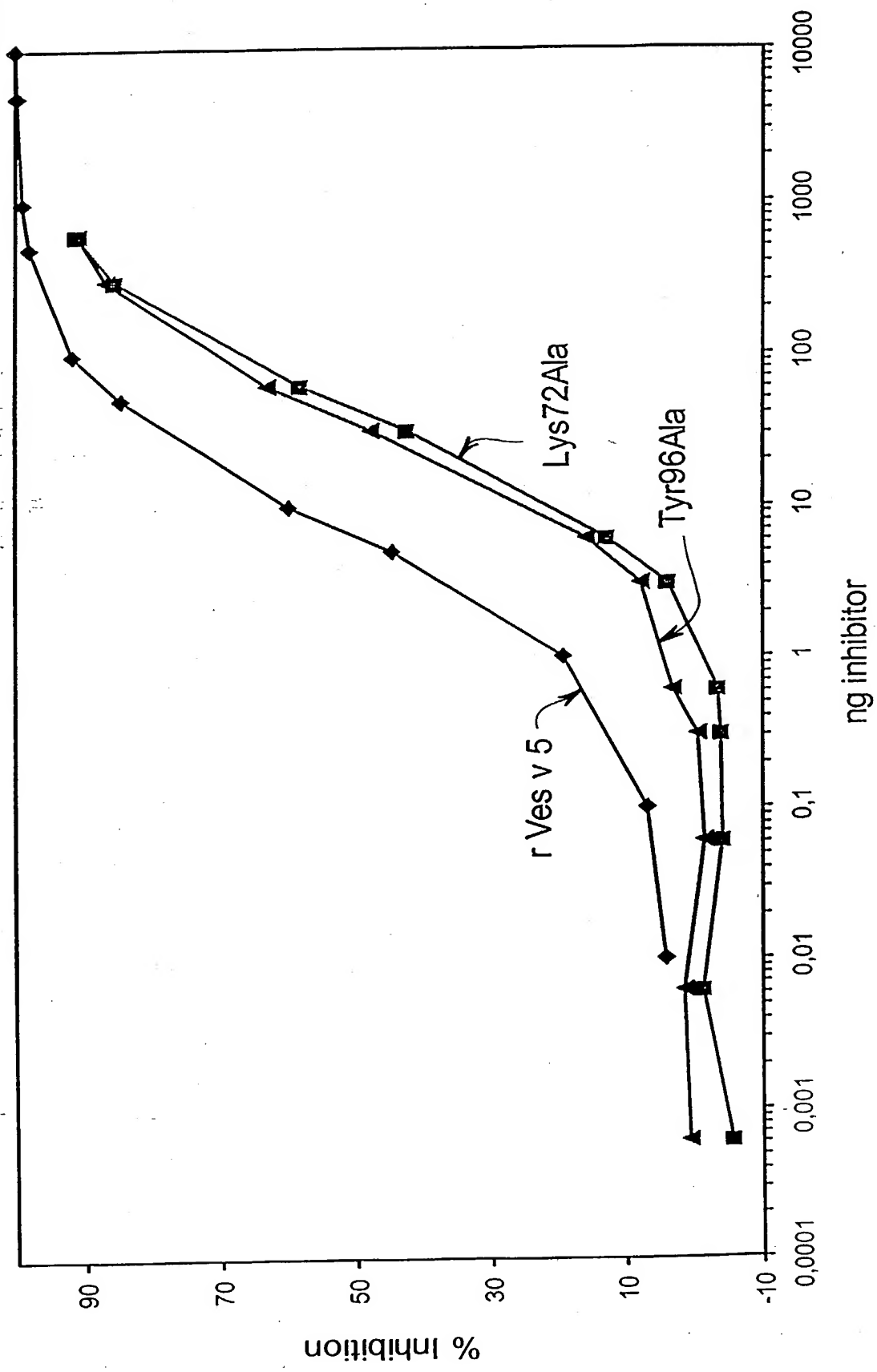
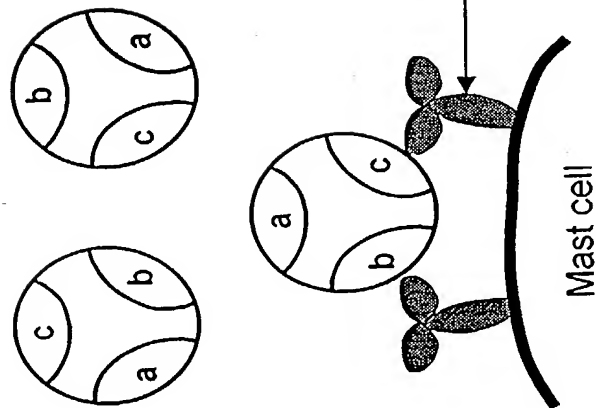
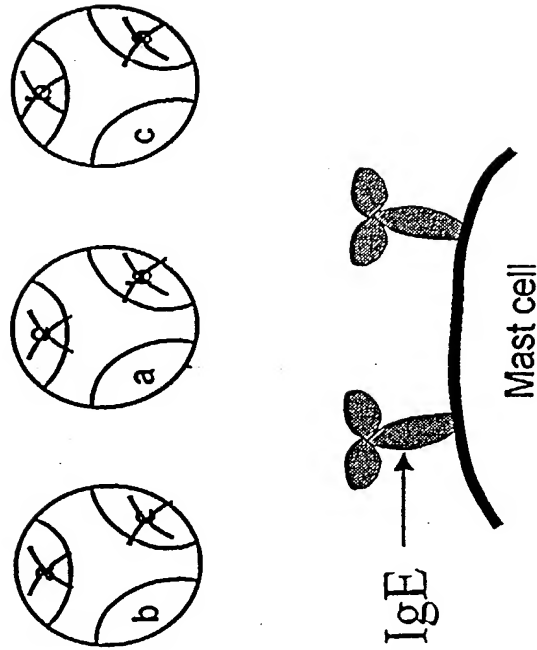


FIG. 15 A



Cross-linking

FIG. 15 B



No cross-linking





## FIG. 16 A

### DNA SEQUENCE

#### ORIGIN

```

1      cacaaattct tcttcttcc ttactactga tcattaatct gaaaacaaaa ccaaacaac
61     catcaaaat gatgtacaaa atttgtgtc tticattgtt ggtcgcagcc gttgctcgtg
121    atcaagtcga tgtcaaagat tgtgccaatc atgaaatcaa aaaagttttg gtaccaggat
181    gccatggttc agaaccatgt atcattcatc gtggtaaacc attccaattg gaagccggtt
241    tcgaagccaa ccaaaacaca aaaacggcta aaattgaaat caaagcctca atcgatggtt
301    tagaagtga tgttcccggt atcgatccaa atgcatgcca tiacatgaaa tgcccattgg
361    ttaaaggaca acaatatgat attaaatata catggaatgt tccgaaaatt gcaccaaaat
421    ctgaaaatgt tgtcgtcact gftaaagfta tgggtgatga tgggtgtttg gcctgtgcta
481    ttgctactca tgctaaaatc cgcgattaaa tcaaacaaaa ttattgatt ttgtaatcac
541    aatgattga ttttcttcc aaaaaaaaaa taaataaaat tttggaatt c

```

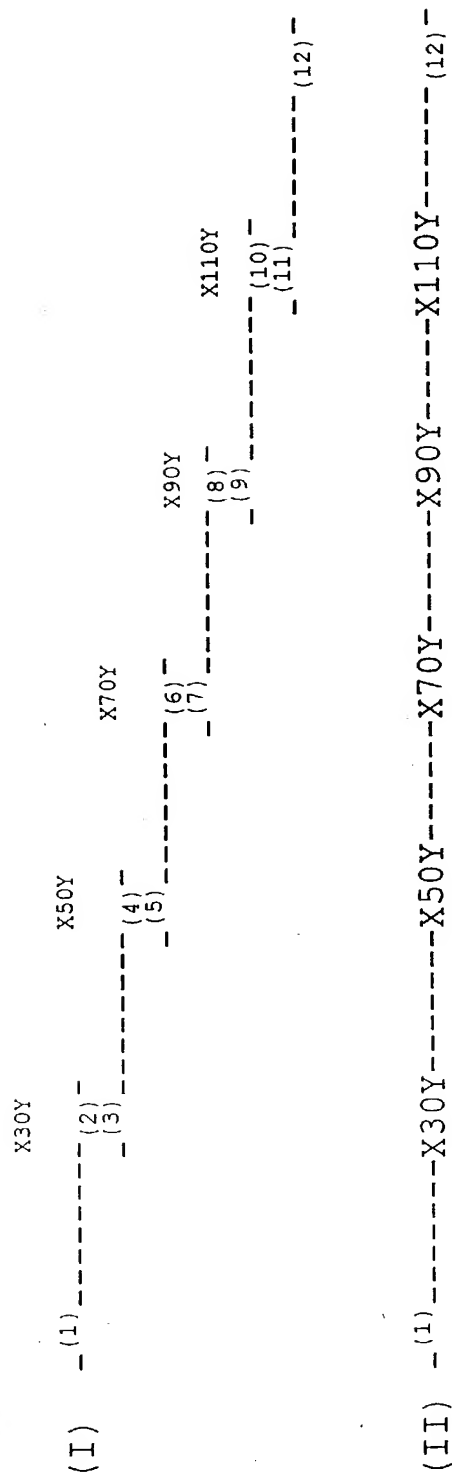
## FIG. 16 B

```

1      mmykilclsl lvaavardqv dvkdcanhei kkvlvpgchg sepciihrhk pfqleavfea
61     nqntktakie ikasidglev dvpgidpnac hymkcplvkg qqydikytwn vpkiapksen
121    vvtvkvmgd dgvlacaiat hakird

```

FIG. 17

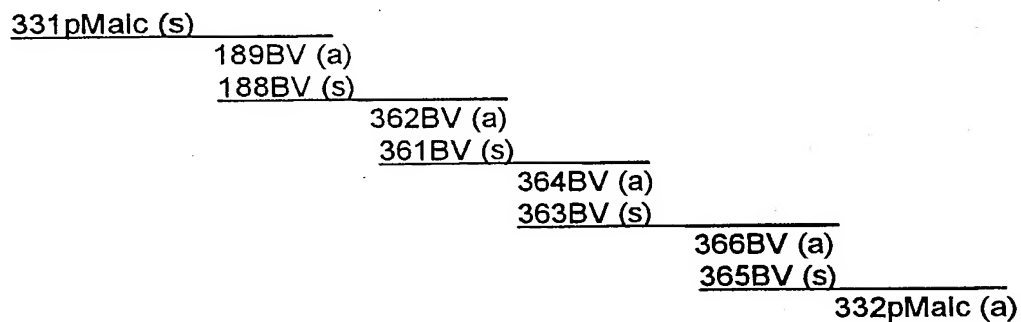


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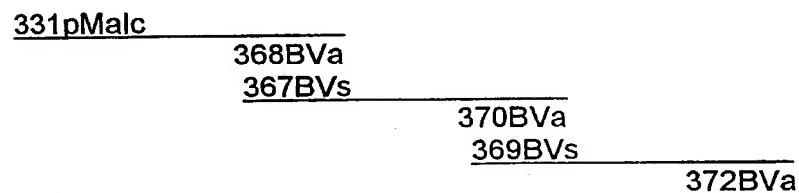
## FIG. 18 A

DNA template: Bet v 1 (2589) carrying the Y5V mutation.



## FIG. 18 B

DNA template: Bet v 1 (2571) carrying N28T, K32Q, P108G mutations.

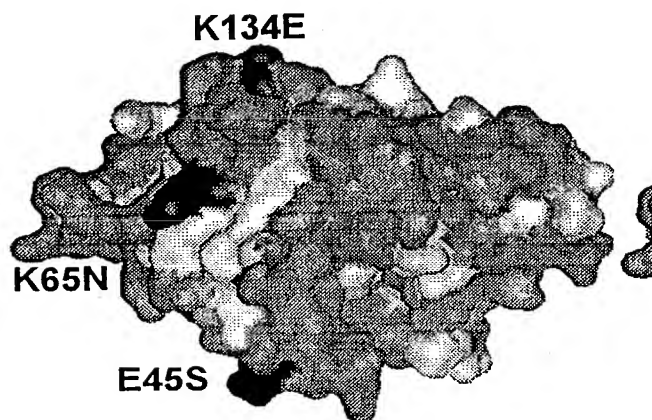
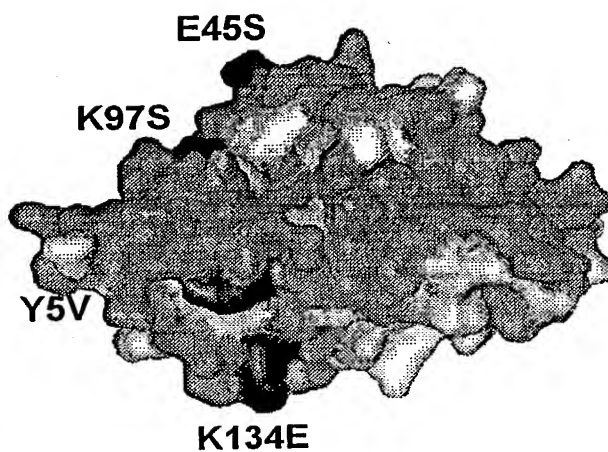
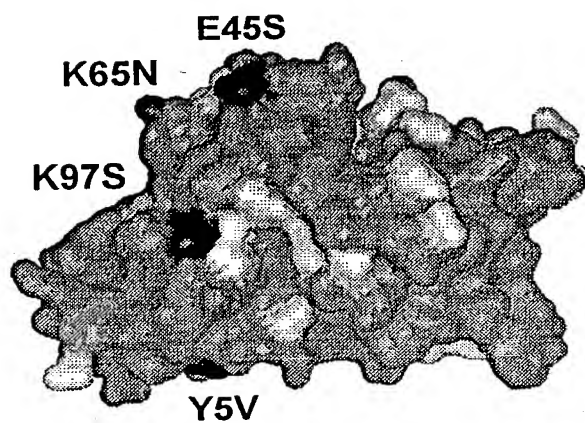


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# FIG. 19 A

Bet v 1 (2628)



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# FIG. 19 B

Bet v 1 (2637)

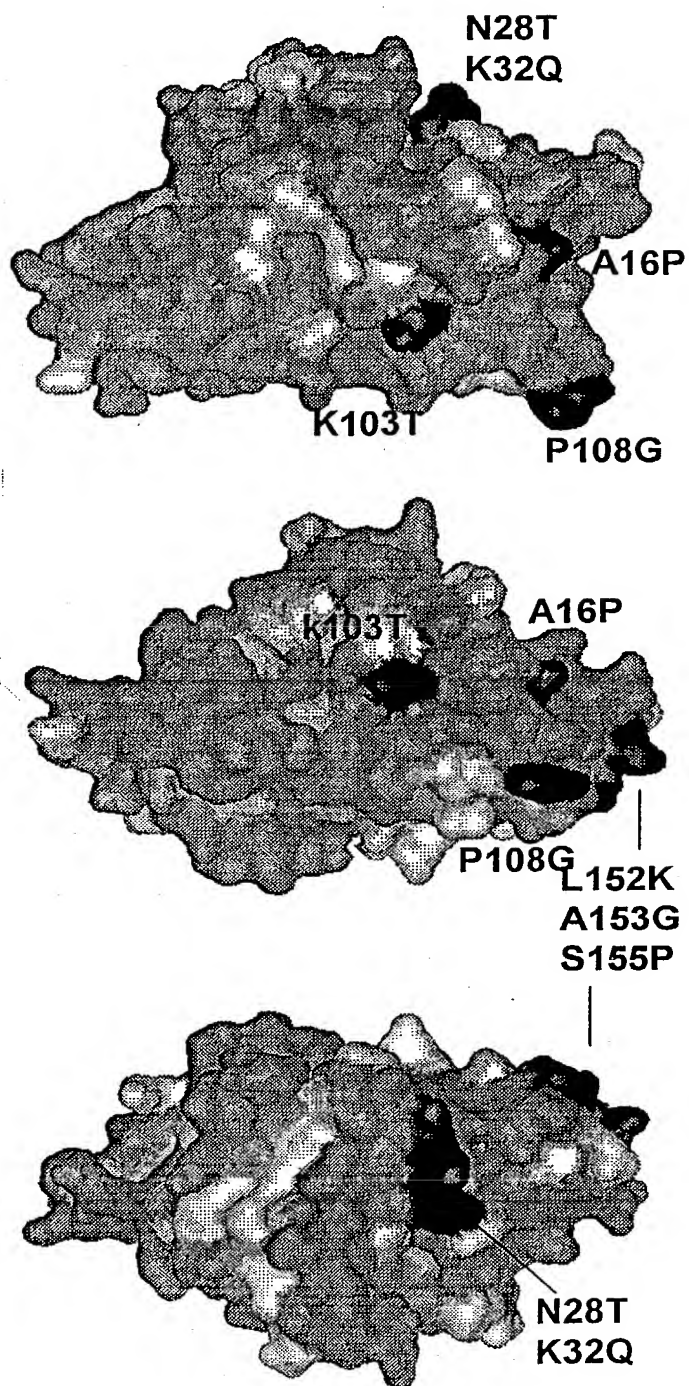
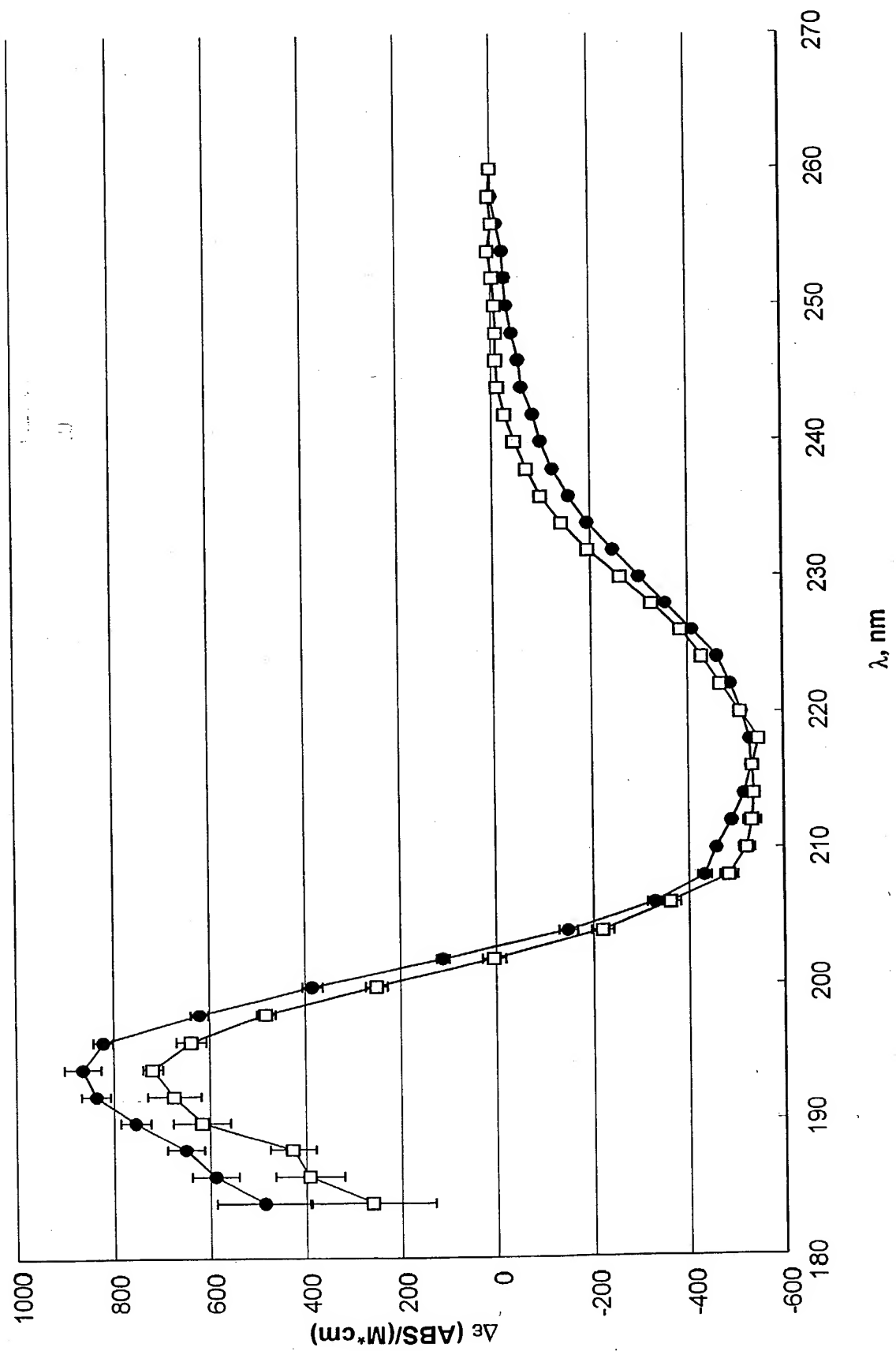






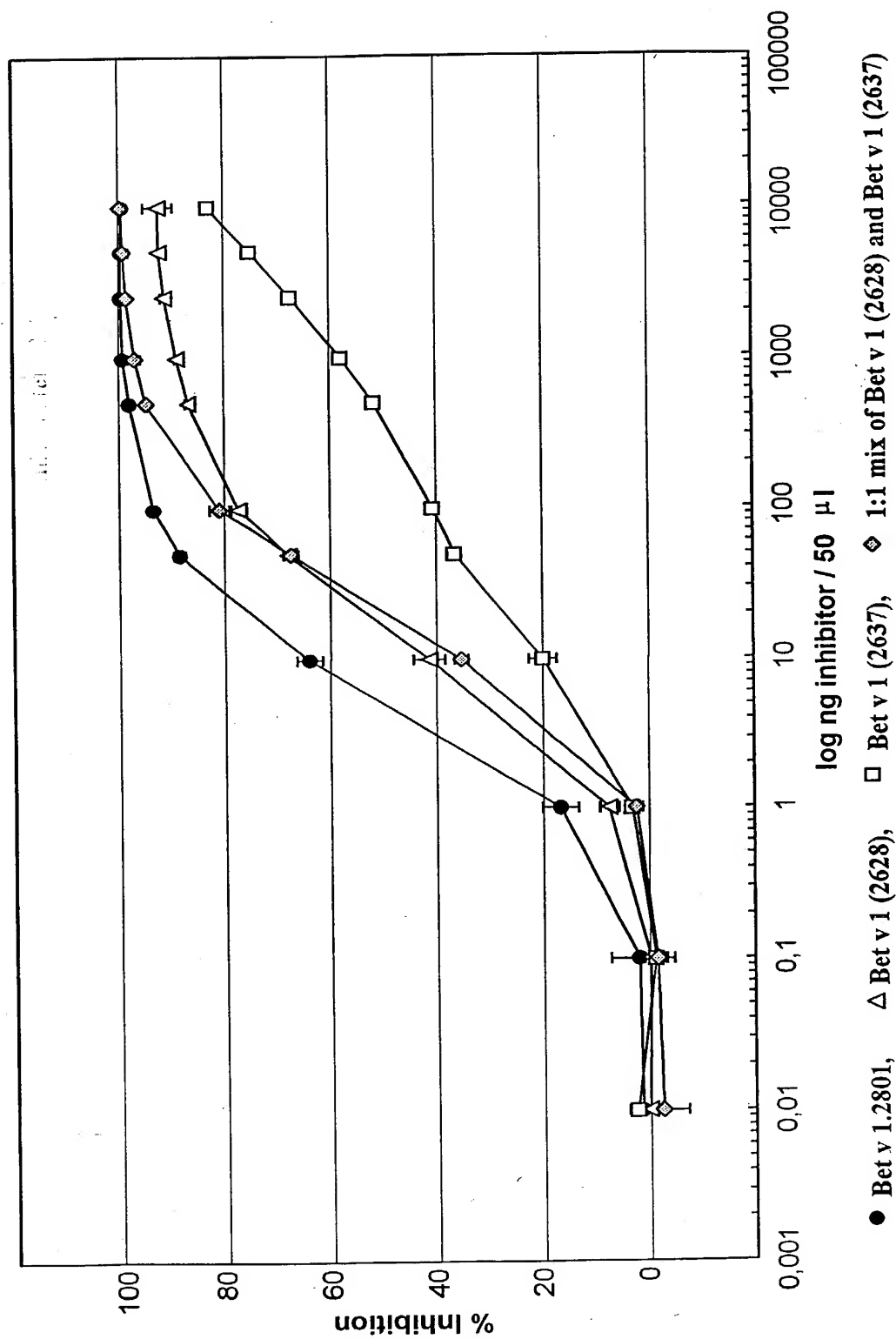
FIG. 20



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FIG. 21



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FIG. 22

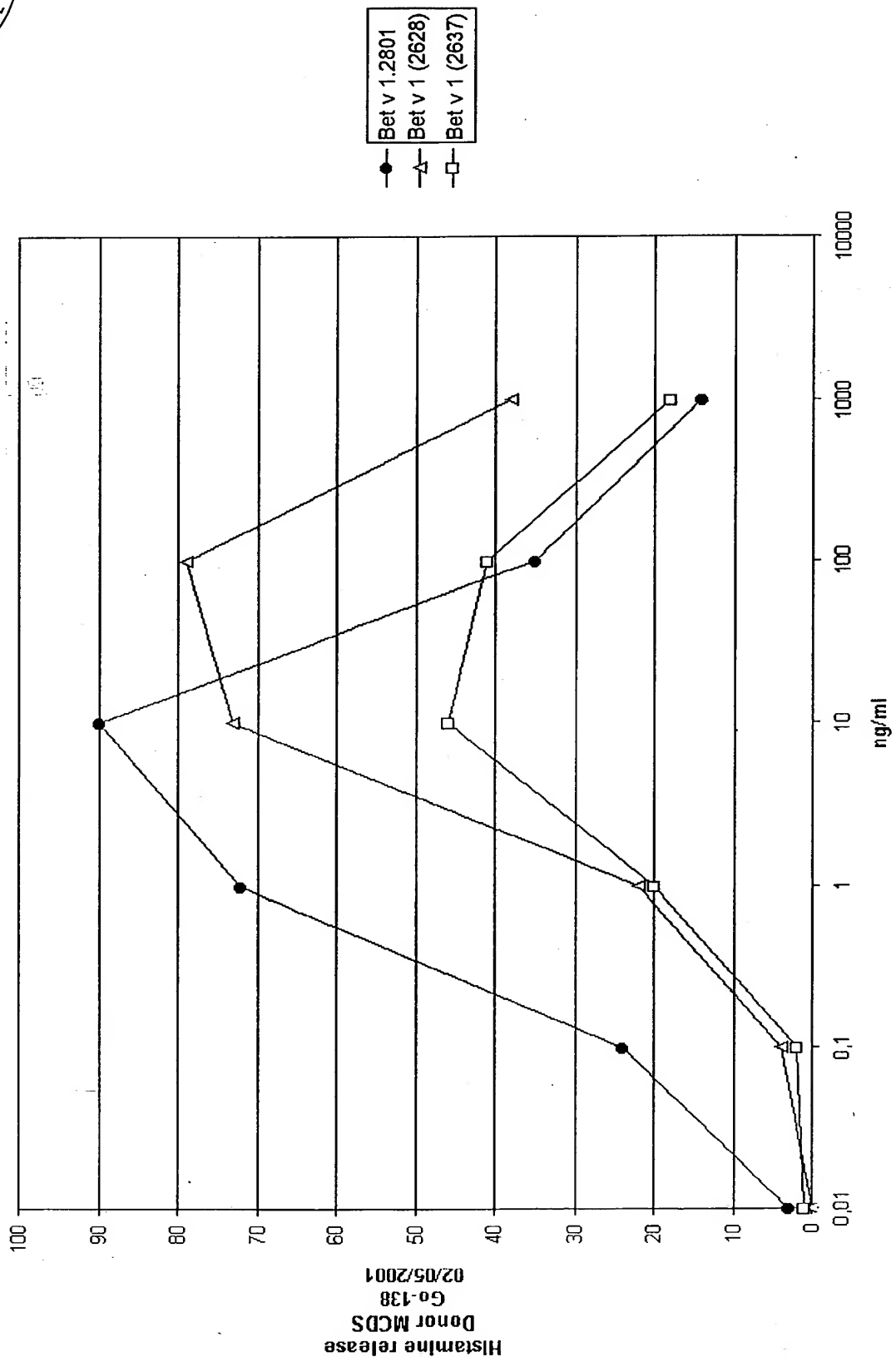


FIG. 23

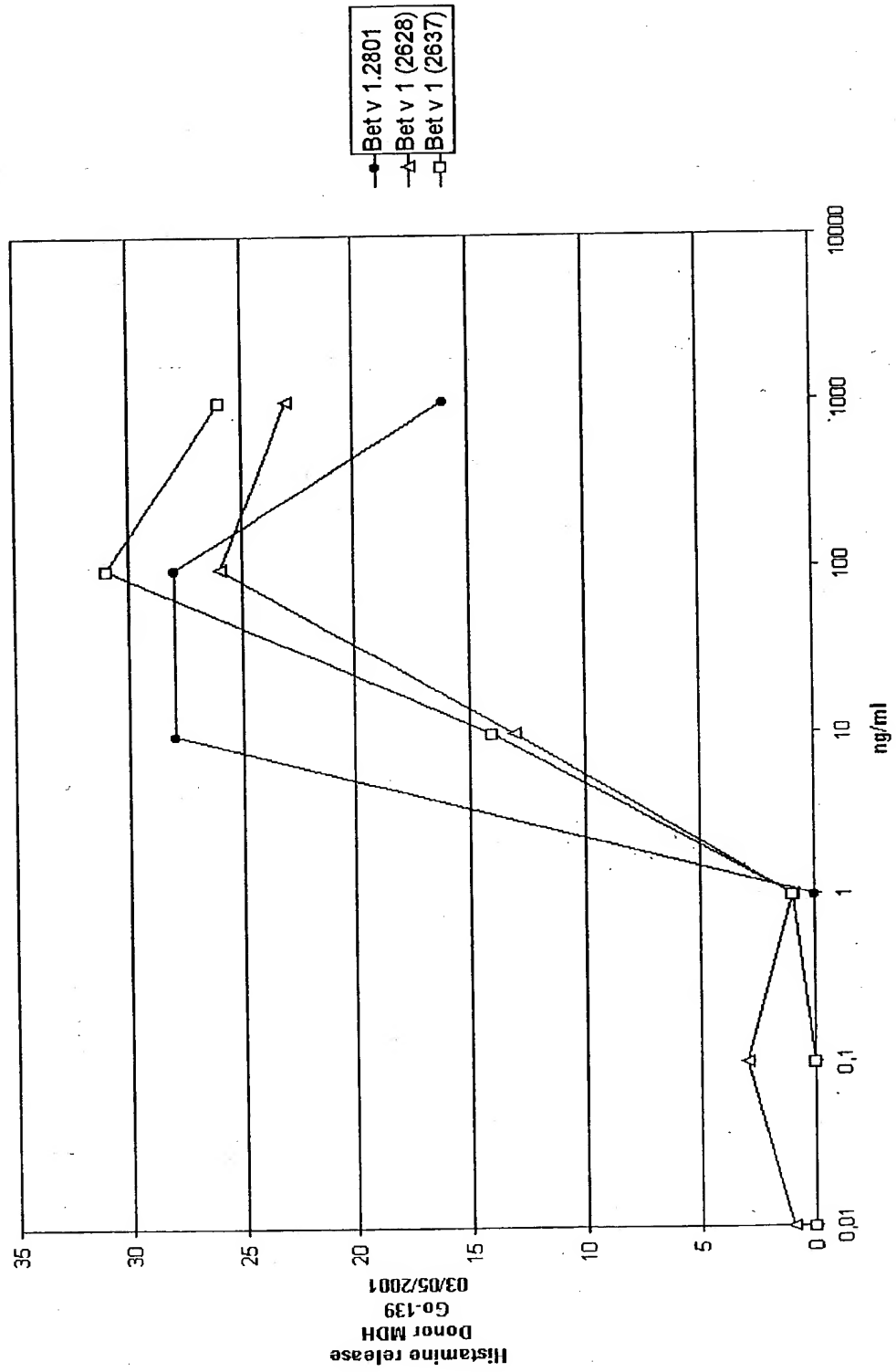
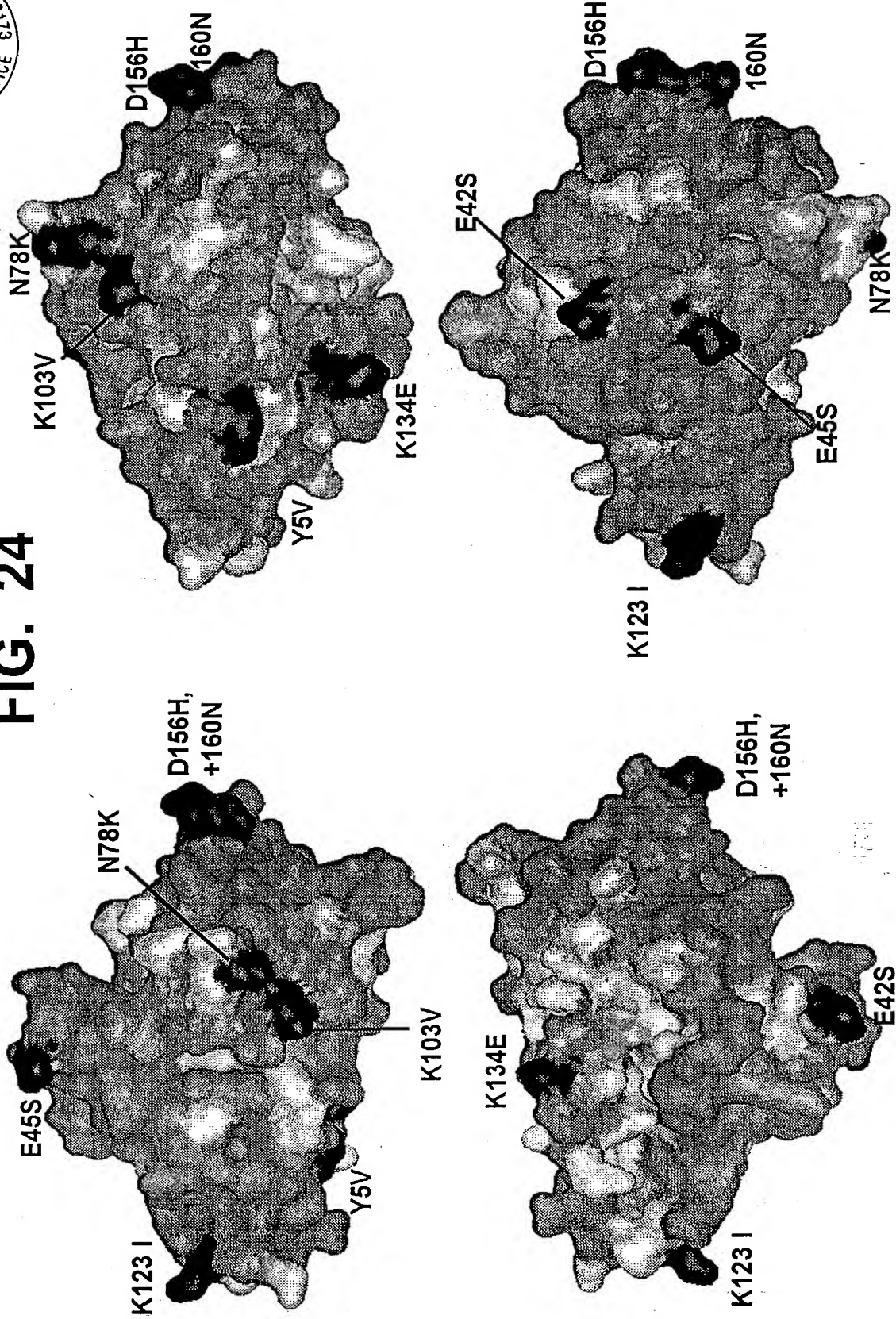


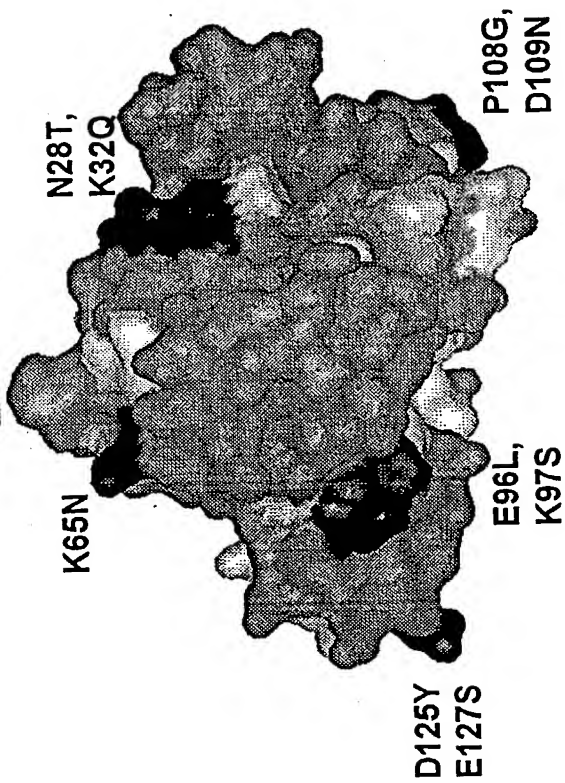
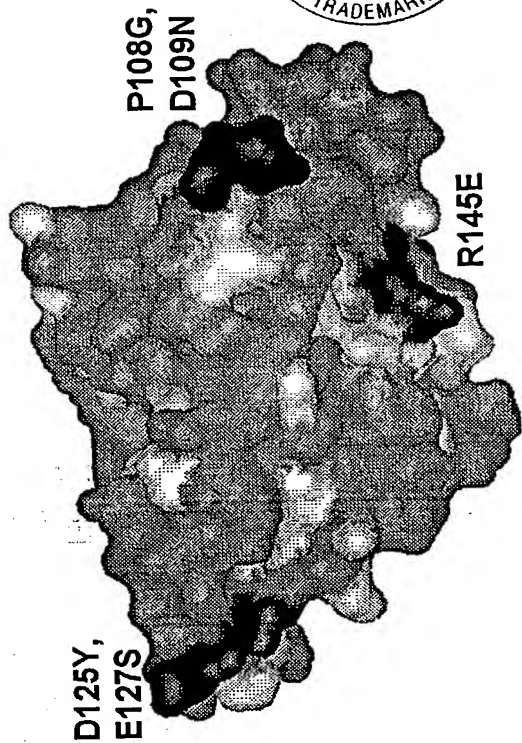
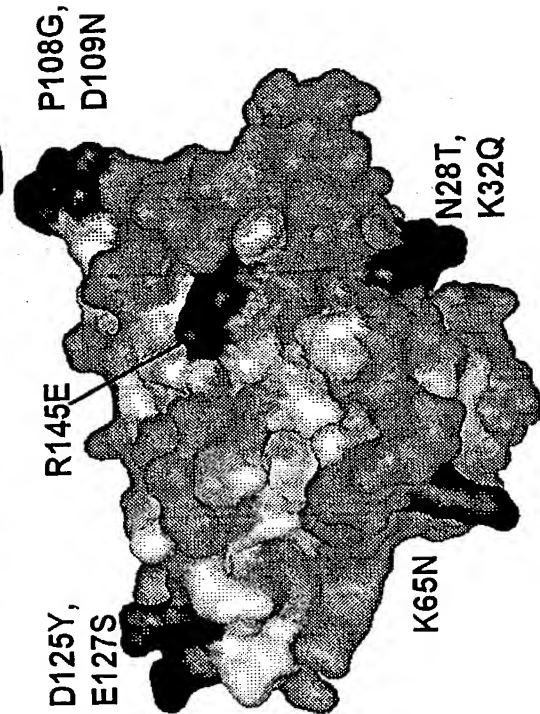
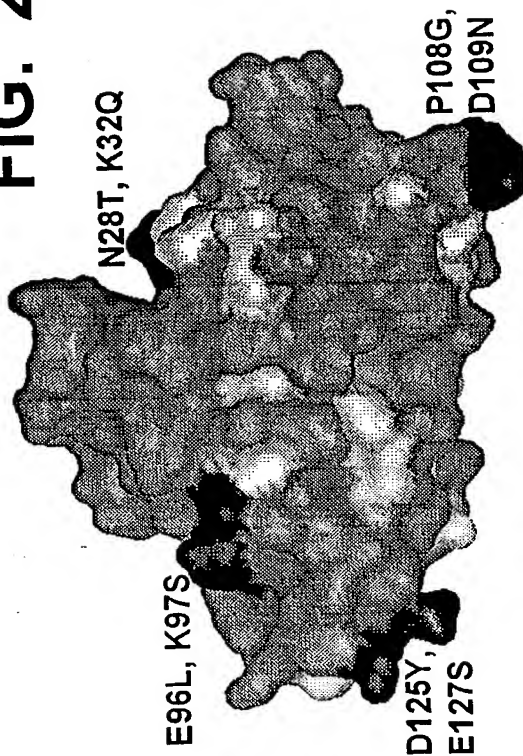
FIG. 24



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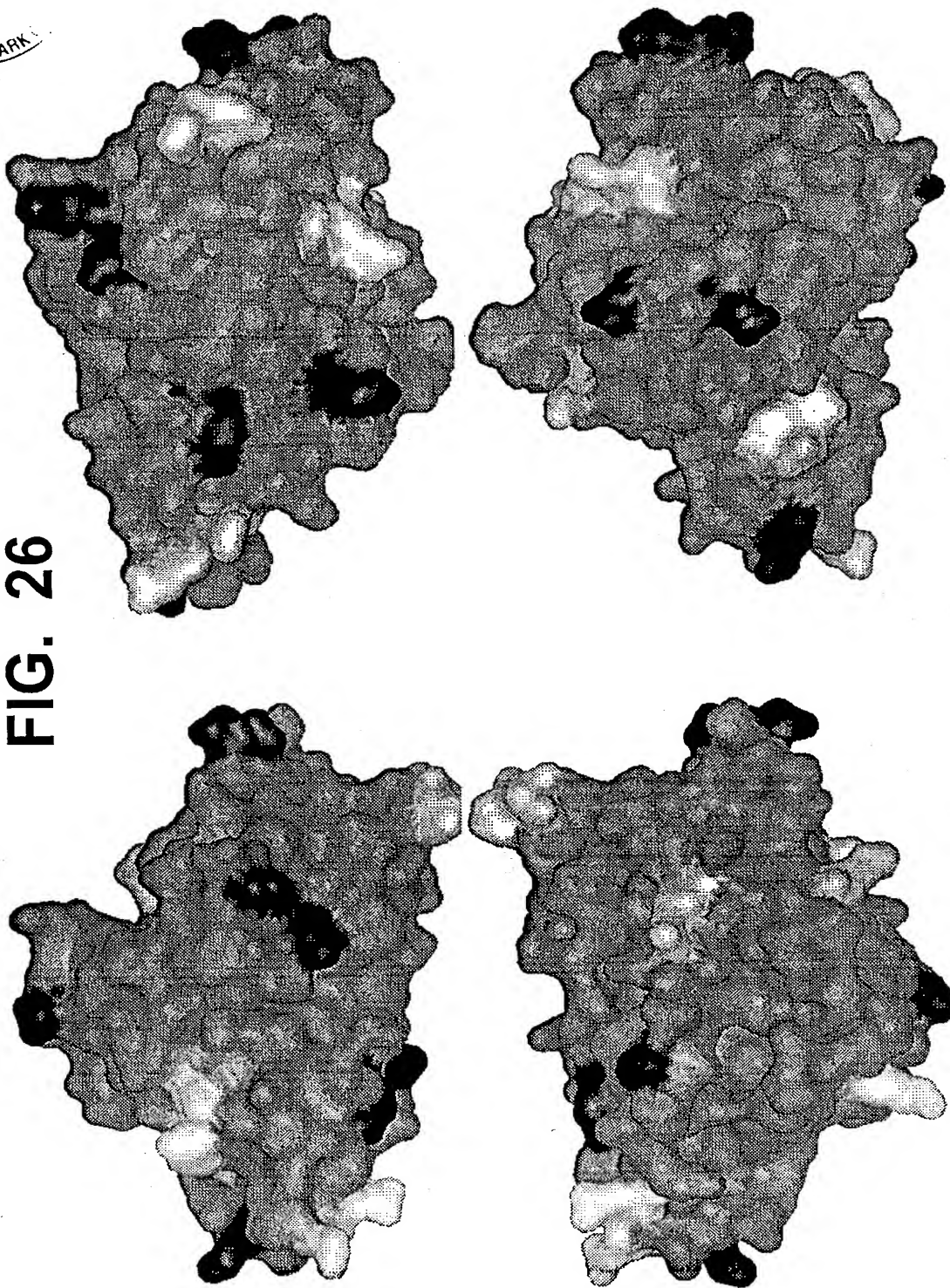
FIG. 25



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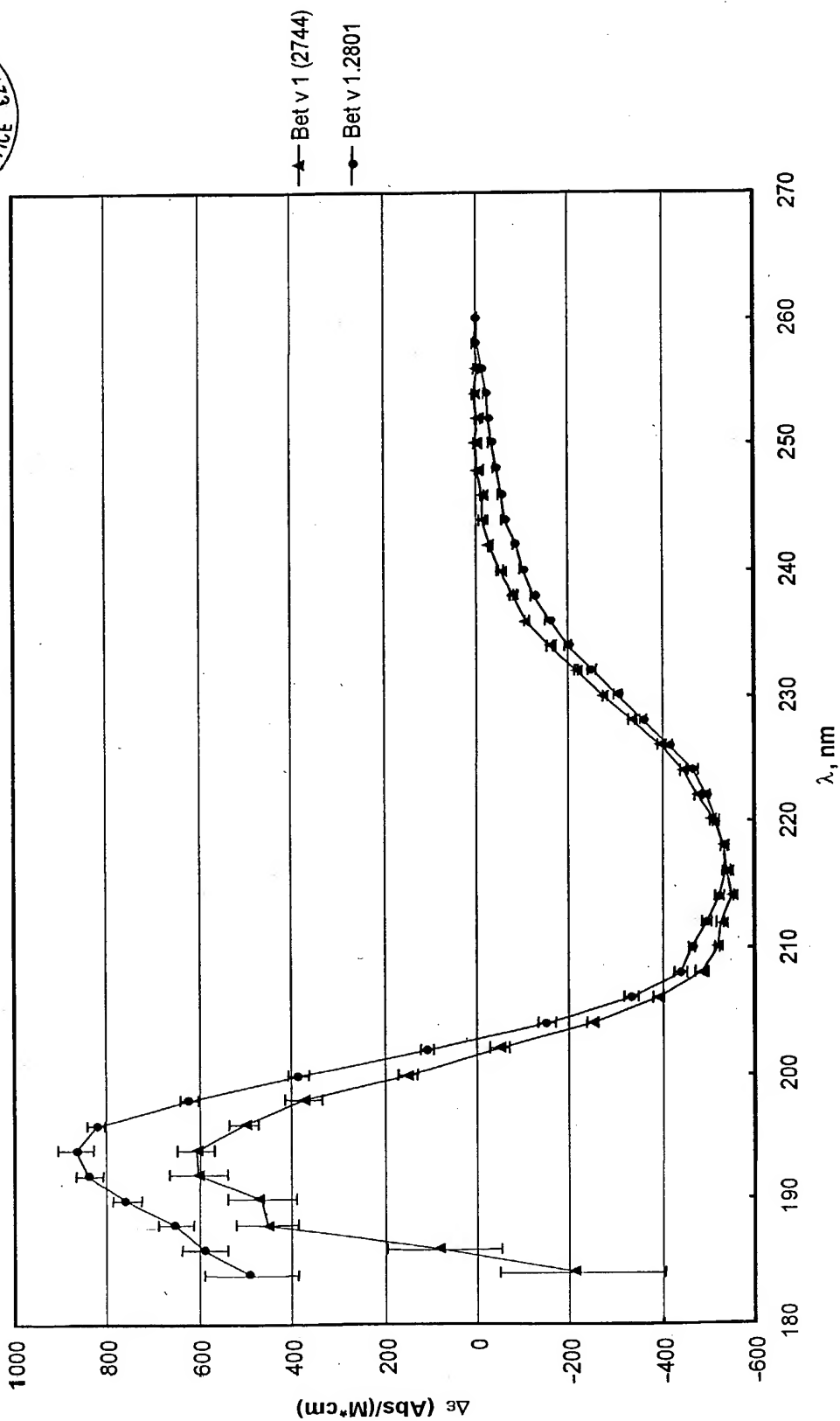
FIG. 26



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FIG. 27

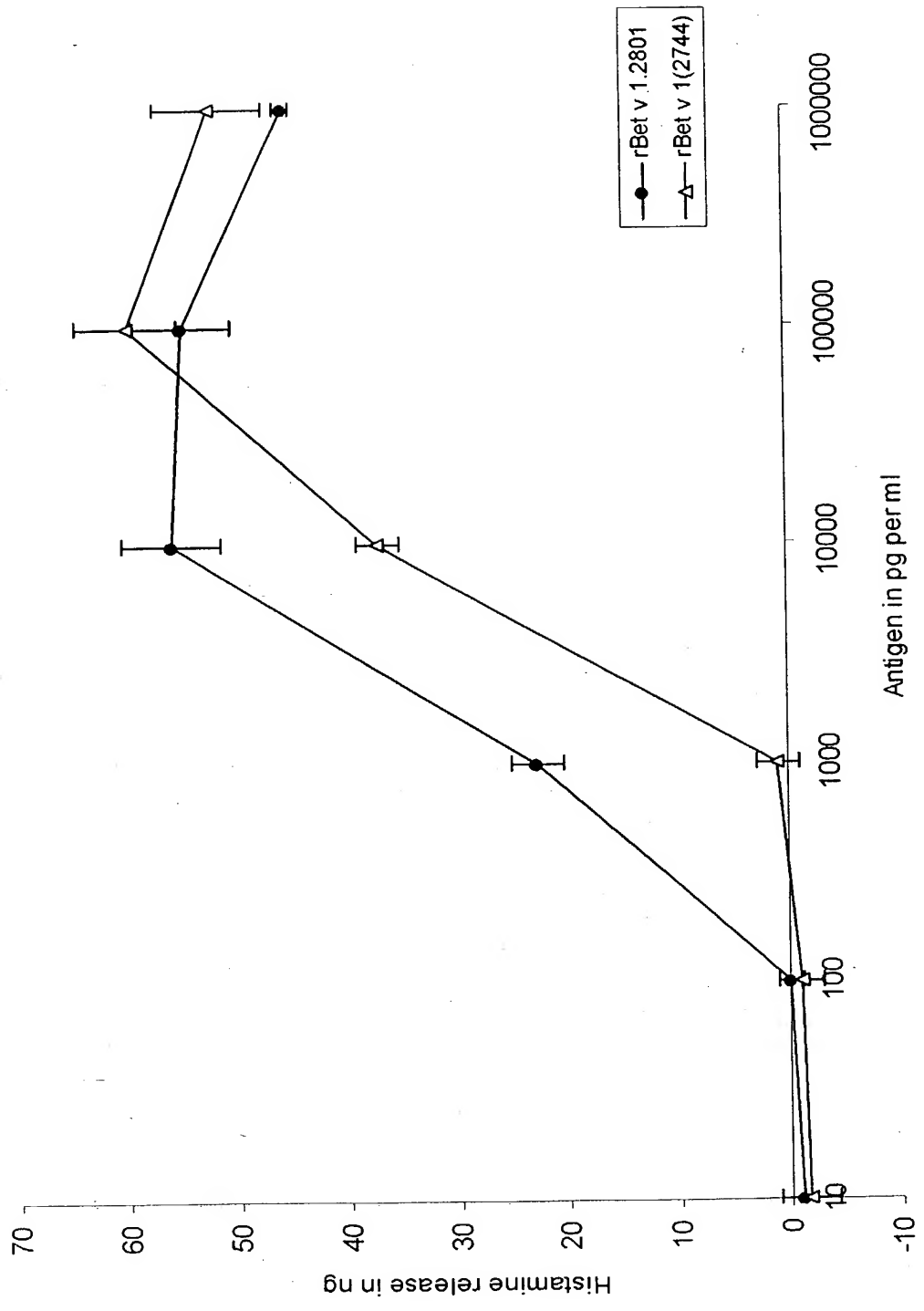




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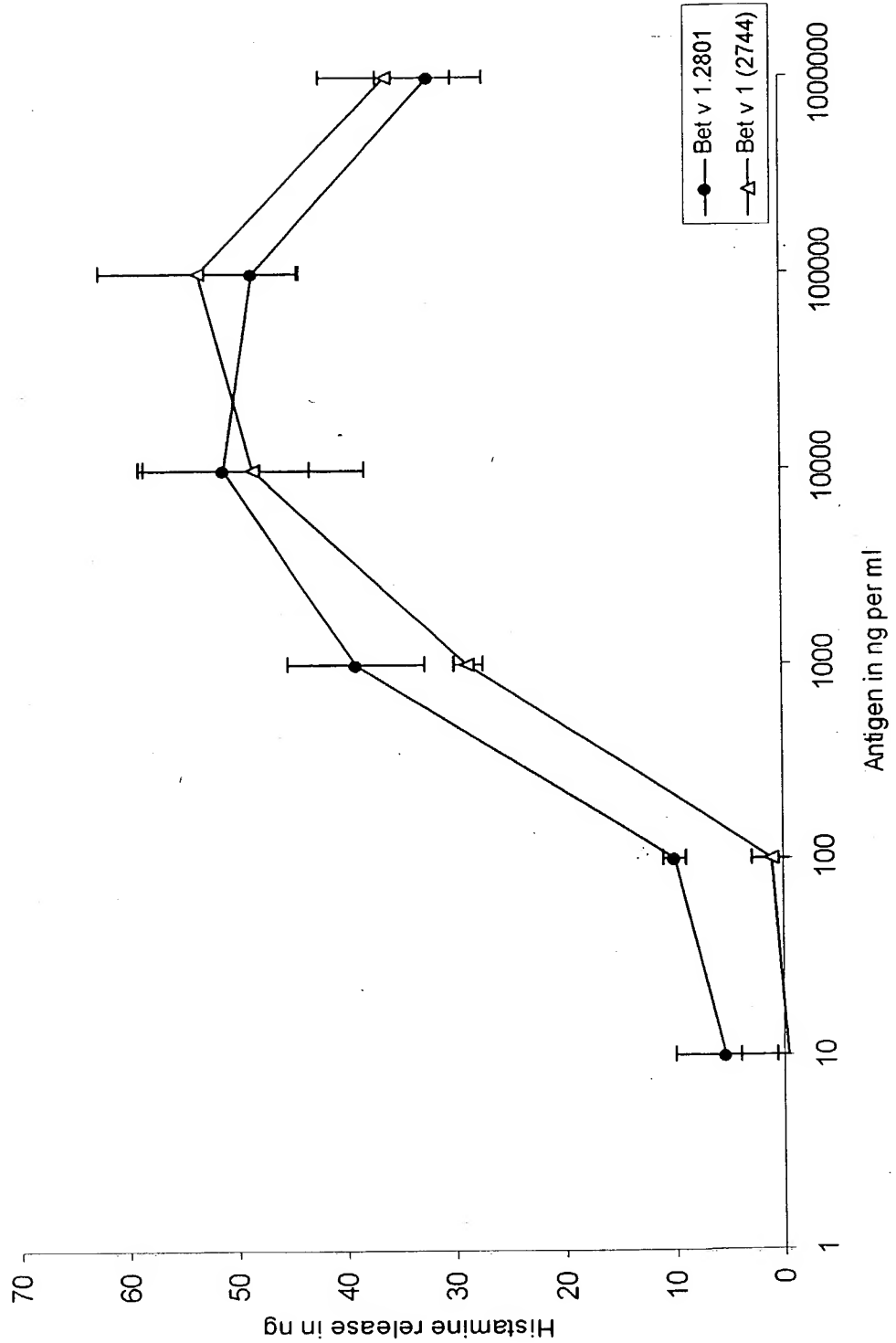
FIG. 28



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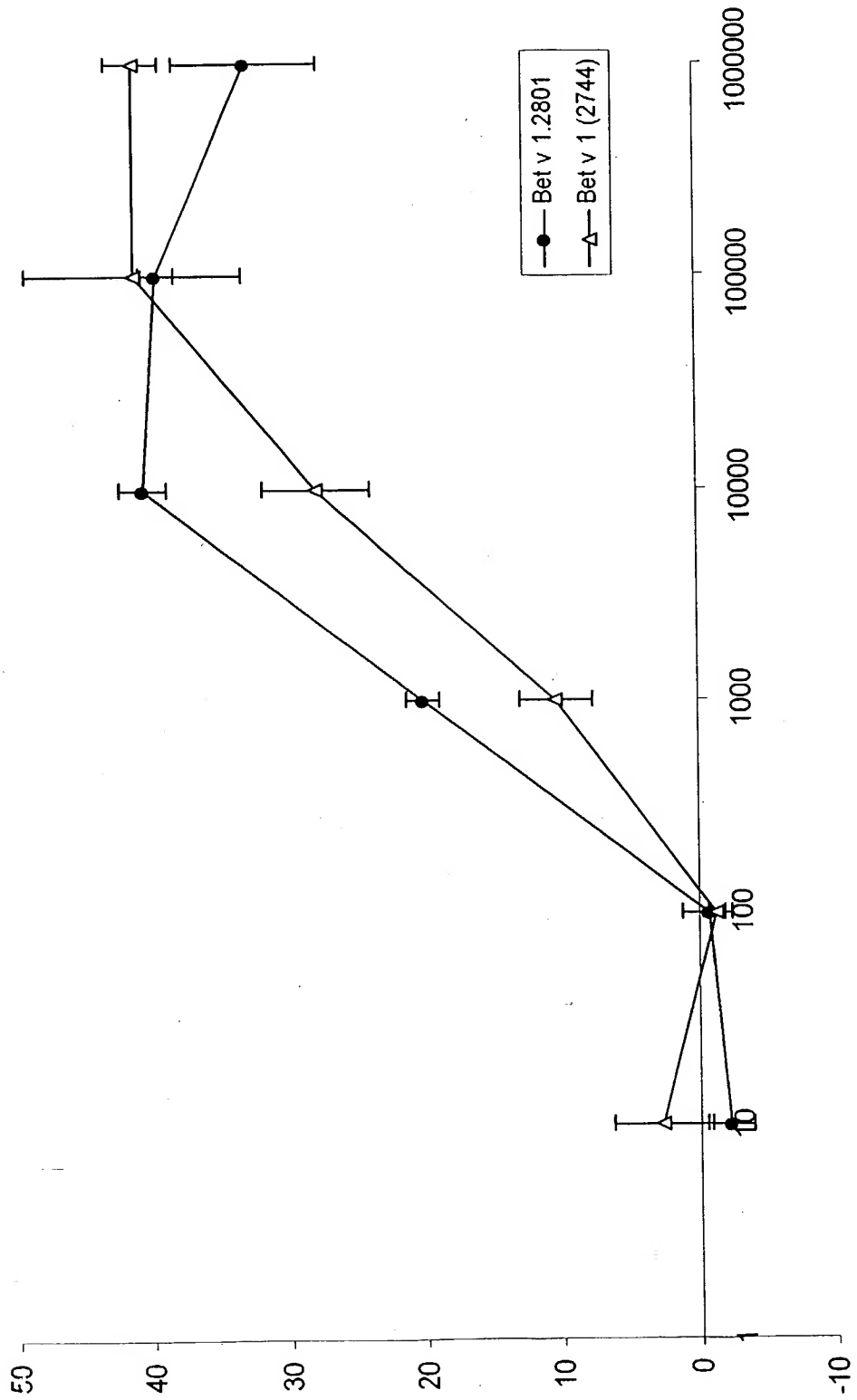
FIG. 29 A



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FIG. 29 B

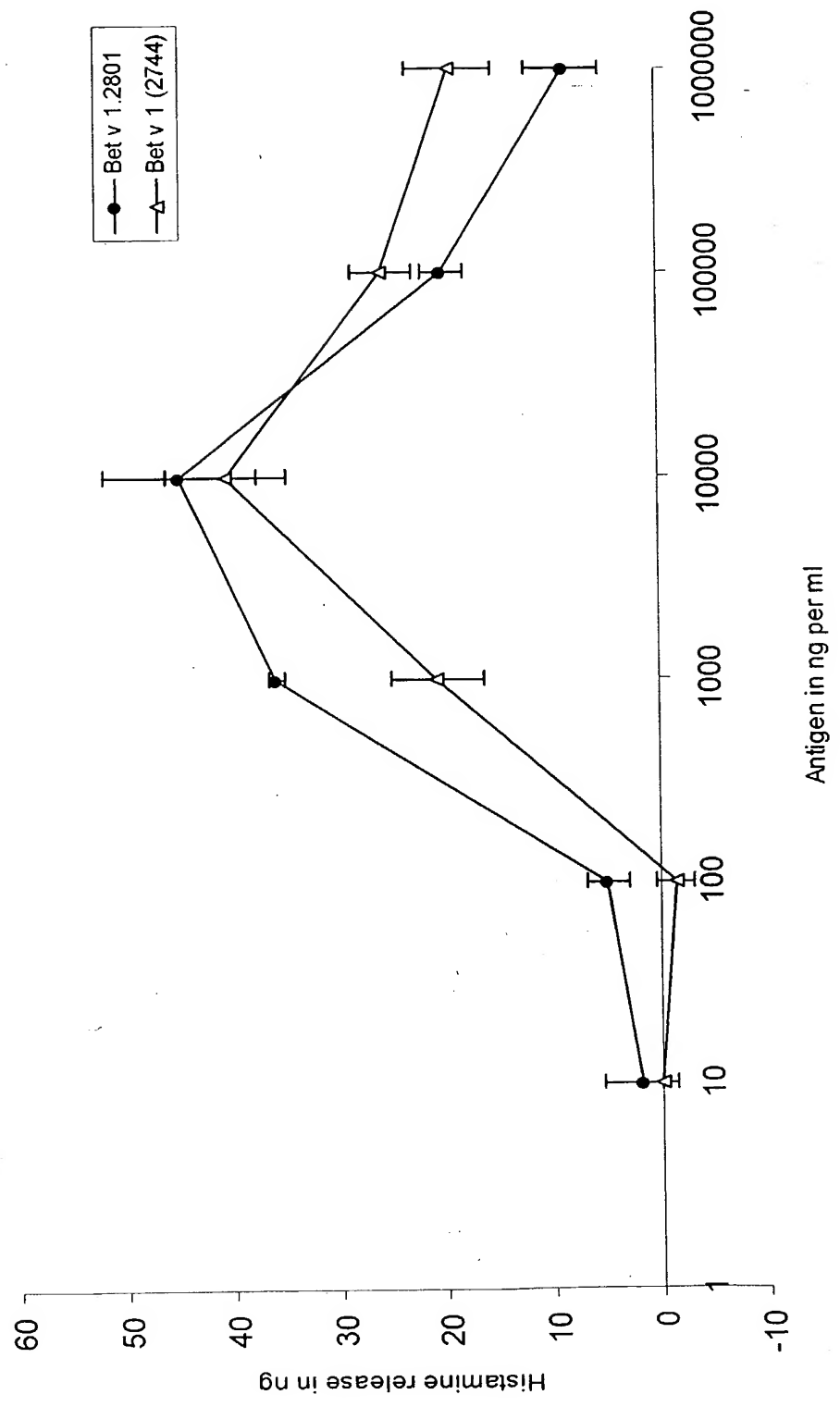


10000000 10000000

10/001,245



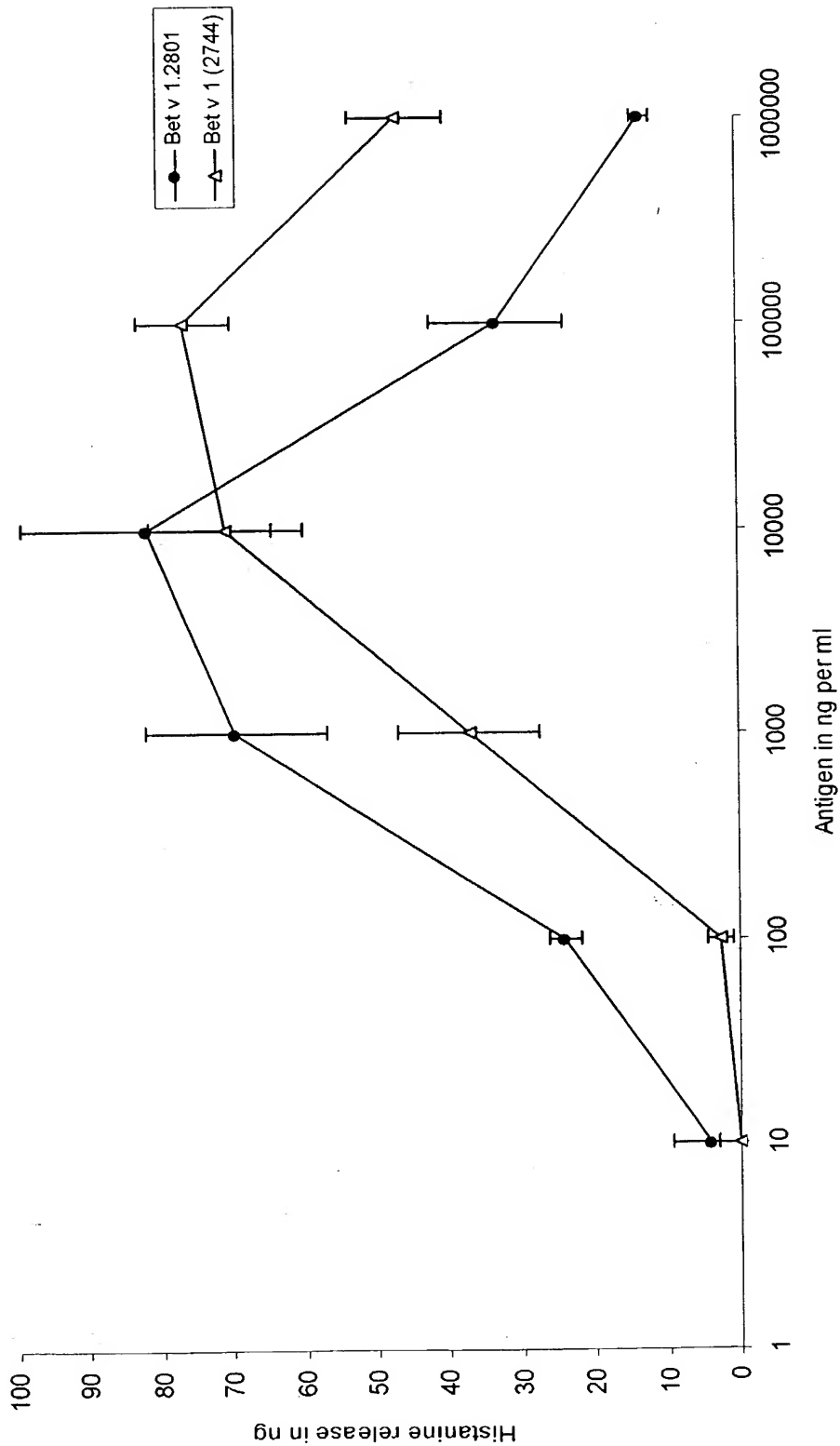
FIG. 29 C



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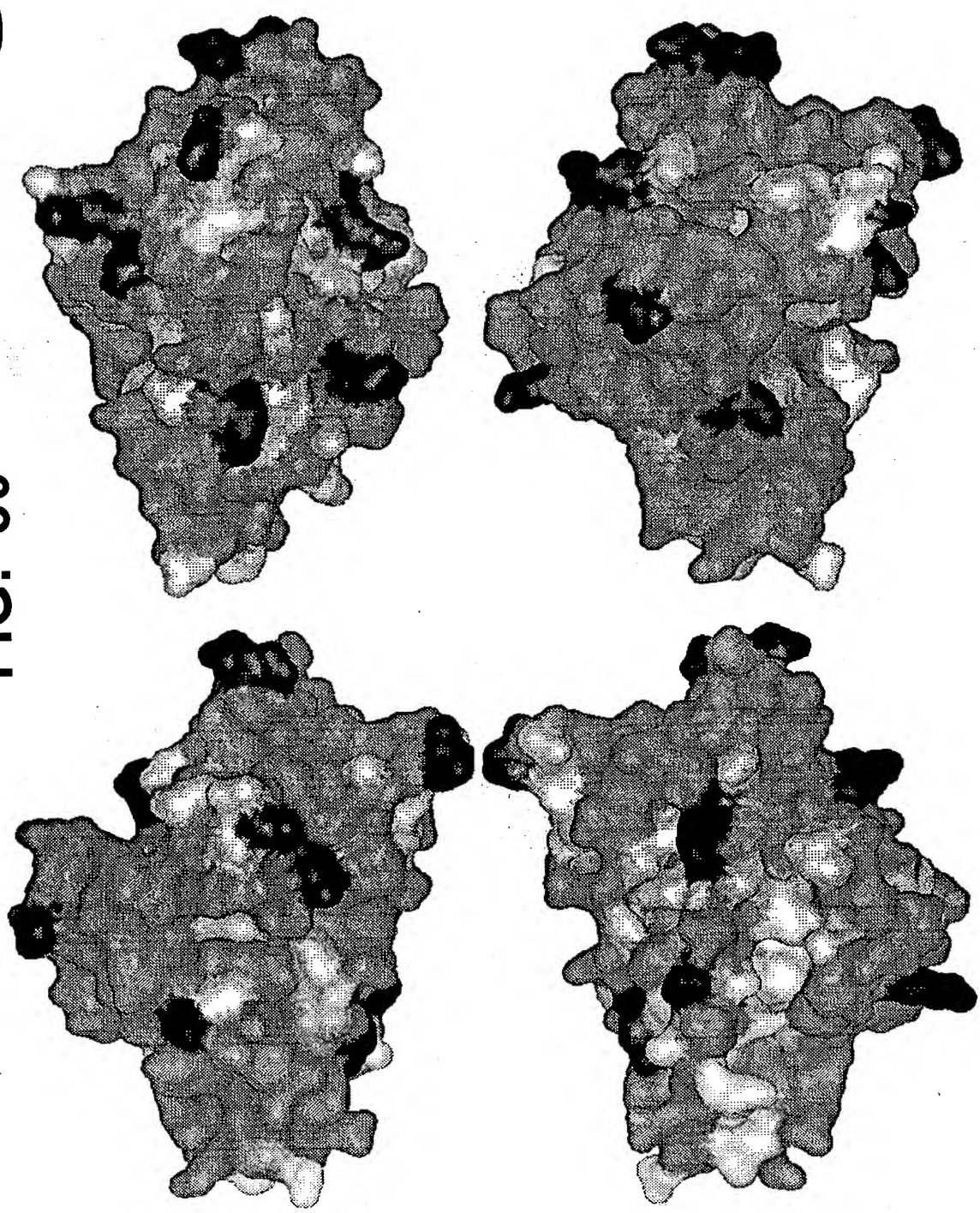
FIG. 29 D



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FIG. 30



## FIG. 31



K6A	sense	OB43	42-mer	5' -CCGCTCGAGAAAAGAGATCAAGTCGATGTCGCCGATTGTGCC-3'
	anti-sense	OB28	39-mer	5' -CGTCTAGACTATTAATCGCGGATTTTAGCATGAGTTGC-3'
K15E	sense	OB44	67-mer	5' -CCGCTCGAGAAAAGAGATCAAGTCGATGTCAAAGATTGTGCC AACCATGAAATCAAAGAAGTTTGG-3'
	anti-sense	OB28	39-mer	5' -CGTCTAGACTATTAATCGCGGATTTTAGCATGAGTTGC-3'
H30N	sense	OB46	54-mer	5' -CGGGTACCAGGATGTCATGGTTCAGAACCATGTATCATTAA CCGTGGTAAACC-3'
	anti-sense	OB28	39-mer	5' -CGTCTAGACTATTAATCGCGGATTTTAGCATGAGTTGC-3'
E62S	sense	OB47	33-mer	5' -GCCTCAATCGATGGTTTATCAGTTGATGTTCCC-3'
	anti-sense	OB48	33-mer	5' -GGGAACATCAACTGATAAACCATCGATTGAGGC-3'
H74N	sense	OB49	32-mer	5' -CATGGCATGCAATTACATGAAATGCCCAATTGG-3'
	anti-sense	OB28	39-mer	5' -CGTCTAGACTATTAATCGCGGATTTTAGCATGAGTTGC-3'
K82N	sense	OB50	50-mer	5' -CTACGCATGCCATTACATGAAATGCCCATTTGGTTAATGGACAA CAATATG-3'
	anti-sense	OB28	39-mer	5' -CGTCTAGACTATTAATCGCGGATTTTAGCATGAGTTGC-3'



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FIG. 32

FIG. 32

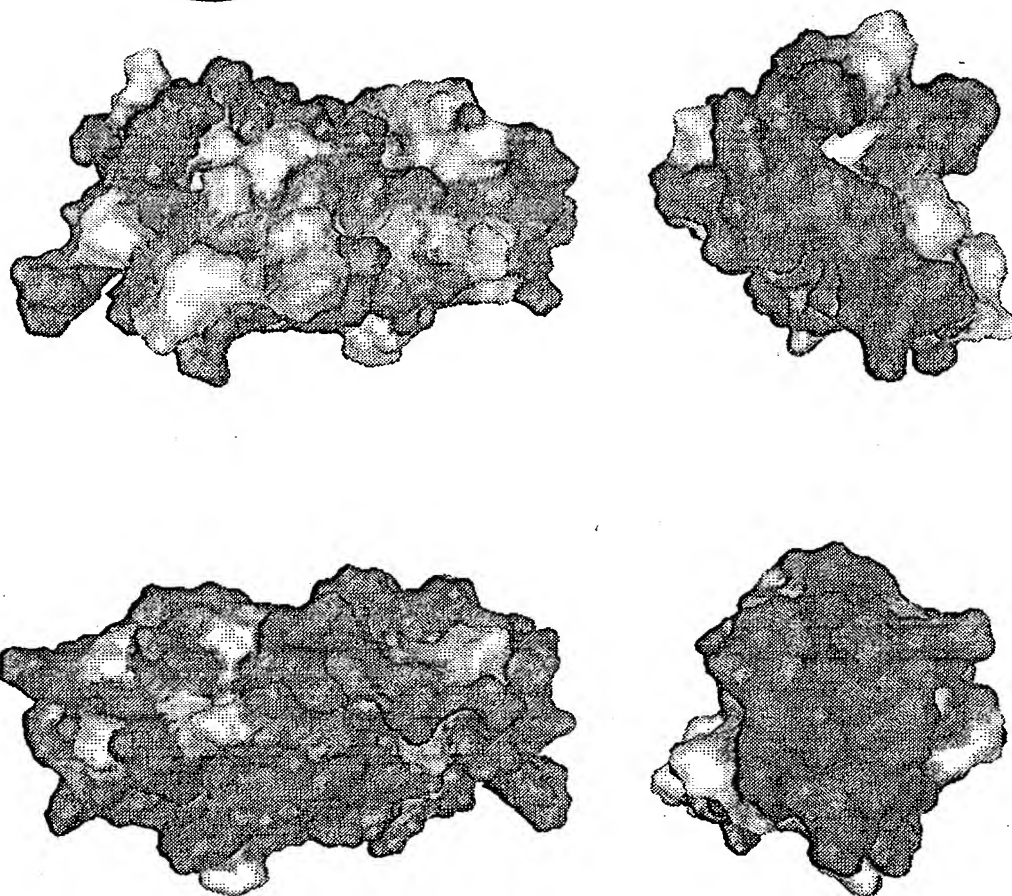
1 DERP2-ALK-G Derp 2	1	10	20	30	
2 DERP 2 CDNA Derp 2	DQVDVKDCANHEIKKVLVPGGCHGSEPCIH				
3 DERP2-ISO101 Derp 2	DQVDVKDCANHEIKKVLVPGGCHGSEPCIH				
4 DERP2-ISO102 Derp 2	DQVDVKDCANHEIKKVLVPGGCHGSEPCIH				
5 DERP2-ISO104 Derp 2	DQVDVKDCANHEIKKVLVPGGCHGSEPCIH				
6 DERP2-ISO113 Derp 2	DQVDVKDCANHEIKKVLVPGGCHGSEPCIH				
7 DERP2-ISO120 Derp 2	DQVDVKDCANHEIKKVLVPGGCHGSEPCIH				
8 1A9V Derp 2	DQVDVKDCANHEIKKVLVPGGCHGSEPCIH				
9 DEF2-DEFA Derf 2	DQVDVKDCANHEIKKVMVVDGCHGSDPCIH				
10 B61241 Derf 2	DQVDVKDCANHEIKKVMVVDGCHGSDPCIH				
11 1AHK Derf 2	DQVDVKDCANHEIKKVMVVDGCHGSDPCIH				
12 A61501 Derf 2	DQVDVKDCANHEIKKVMVVDGCHGSDPCIH				
13 O96430 Eur m 2 0101 O96430	DQVDVKDCANHEIKKVMVVDGCKGSEPCVIH				
14 O917ZZ Eur m 2 0102 O917ZZ	DQVDVKDCANHEIKKVMVVDGCKGSEPCVIH				
1 DERP2-ALK-G Derp 2	40	50	60	70	80
2 DERP 2 CDNA Derp 2	RGKPFQLEALVFEEANQNTKTAKIEIKASIDGLEVDVPGIDPNACHYHMKCPL				
3 DERP2-ISO101 Derp 2	RGKPFQLEALVFEEANQNTKTAKIEIKASIDGLEVDVPGIDPNACHYHMKCPL				
4 DERP2-ISO102 Derp 2	RGKPFQLEALVFEEANQNTKTAKIEIKASIDGLEVDVPGIDPNACHYHMKCPL				
5 DERP2-ISO104 Derp 2	RGKPFQLEALVFEEANQNTKTAKIEIKASIDGLEVDVPGIDPNACHYHMKCPL				
6 DERP2-ISO113 Derp 2	RGKPFQLEALVFEEANQNTKTAKIEIKASIDGLEVDVPGIDPNACHYHMKCPL				
7 DERP2-ISO120 Derp 2	RGKPFQLEALVFEEANQNTKTAKIEIKASIDGLEVDVPGIDPNACHYHMKCPL				
8 1A9V Derp 2	RGKPFQLEALVFEEANQNTKTAKIEIKASIDGLEVDVPGIDPNACHYHMKCPL				
9 DEF2-DEFA Derf 2	RGKPFQLEALVFEEANQNTKTAKIEIKASIDGLEVDVPGIDPNACHYHMKCPL				
10 B61241 Derf 2	RGKPFQLEALVFEEANQNTKTAKIEIKASIDGLEVDVPGIDPNACHYHMKCPL				
11 1AHK Derf 2	RGKPFQLEALVFEEANQNTKTAKIEIKASIDGLEVDVPGIDPNACHYHMKCPL				
12 A61501 Derf 2	RGKPFQLEALVFEEANQNTKTAKIEIKASIDGLEVDVPGIDPNACHYHMKCPL				
13 O96430 Eur m 2 0101 O96430	RGTAFFQLEALVFEEANQNSNAKIEIKATIDGVVEIDVPGIDNHLCHFHMKCPL				
14 O917ZZ Eur m 2 0102 O917ZZ	RGTAFFQLEALVFEEANQNSNAKIEIKATIDGVVEIDVPGIDNHLCHFHMKCPL				
1 DERP2-ALK-G Derp 2	90	100	110	120	
2 DERP 2 CDNA Derp 2	VKGQQYDICKYTWNVPKIAPKSENVVVTVKVLLGDNGLVLAACAIATHAKIRRD				
3 DERP2-ISO101 Derp 2	VKGQQYDICKYTWNVPKIAPKSENVVVTVKVLLGDNGLVLAACAIATHAKIRRD				
4 DERP2-ISO102 Derp 2	VKGQQYDICKYTWNVPKIAPKSENVVVTVKVLLGDNGLVLAACAIATHAKIRRD				
5 DERP2-ISO104 Derp 2	VKGQQYDICKYTWNVPKIAPKSENVVVTVKVLLGDNGLVLAACAIATHAKIRRD				
6 DERP2-ISO113 Derp 2	VKGQQYDICKYTWNVPKIAPKSENVVVTVKVLLGDNGLVLAACAIATHAKIRRD				
7 DERP2-ISO120 Derp 2	VKGQQYDICKYTWNVPKIAPKSENVVVTVKVLLGDNGLVLAACAIATHAKIRRD				
8 1A9V Derp 2	VKGQQYDICKYTWNVPKIAPKSENVVVTVKVLLGDNGLVLAACAIATHAKIRRD				
9 DEF2-DEFA Derf 2	VKGQQYDICKYTWNVPKIAPKSENVVVTVKVLLGDNGLVLAACAIATHAKIRRD				
10 B61241 Derf 2	VKGQQYDICKYTWNVPKIAPKSENVVVTVKVLLGDNGLVLAACAIATHAKIRRD				
11 1AHK Derf 2	VKGQQYDICKYTWNVPKIAPKSENVVVTVKVLLGDNGLVLAACAIATHAKIRRD				
12 A61501 Derf 2	VKGQQYDICKYTWNVPKIAPKSENVVVTVKVLLGDNGLVLAACAIATHAKIRRD				
13 O96430 Eur m 2 0101 O96430	VKGQEQYDICKYTWNVPRIPAKSENVVVTVKLLGDNGLVLAACAIATHAKIRRD				
14 O917ZZ Eur m 2 0102 O917ZZ	VKGQEQYDICKYTWNVPRIPAKSENVVVTVKLLGDNGLVLAACAIATHAKIRRD				



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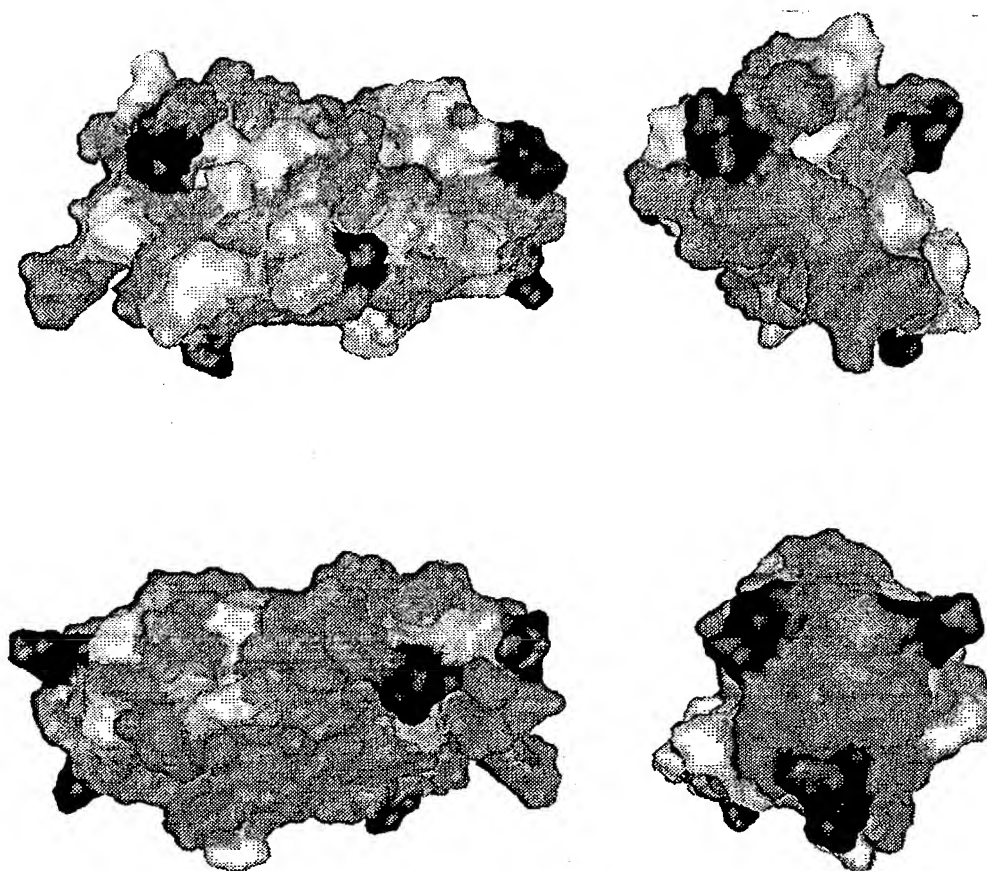
**FIG. 33**



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**FIG. 34**



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FIG. 35 A

	1 0 0	9 0	8 0	7 0	6 0	5 0	
Derp1 AUK							
Derp1							
Eurm 1.0101							
Eurm 1.0101							
Eurm 1.0102							
Derf1							
Eurm 1							
Derf1							
	4 0	3 0	2 0	1 0	1	1 0	
Derp1 AUK							
Derp1							
Eurm 1.0101							
Eurm 1.0101							
Eurm 1.0102							
Derf1							
Eurm 1							
Derf1							
	2 0	3 0	4 0	5 0	6 0	7 0	
Derp1 AUK							
Derp1							
Eurm 1.0101							
Eurm 1.0101							
Eurm 1.0102							
Derf1							
Eurm 1							
Derf1							

10/001,245



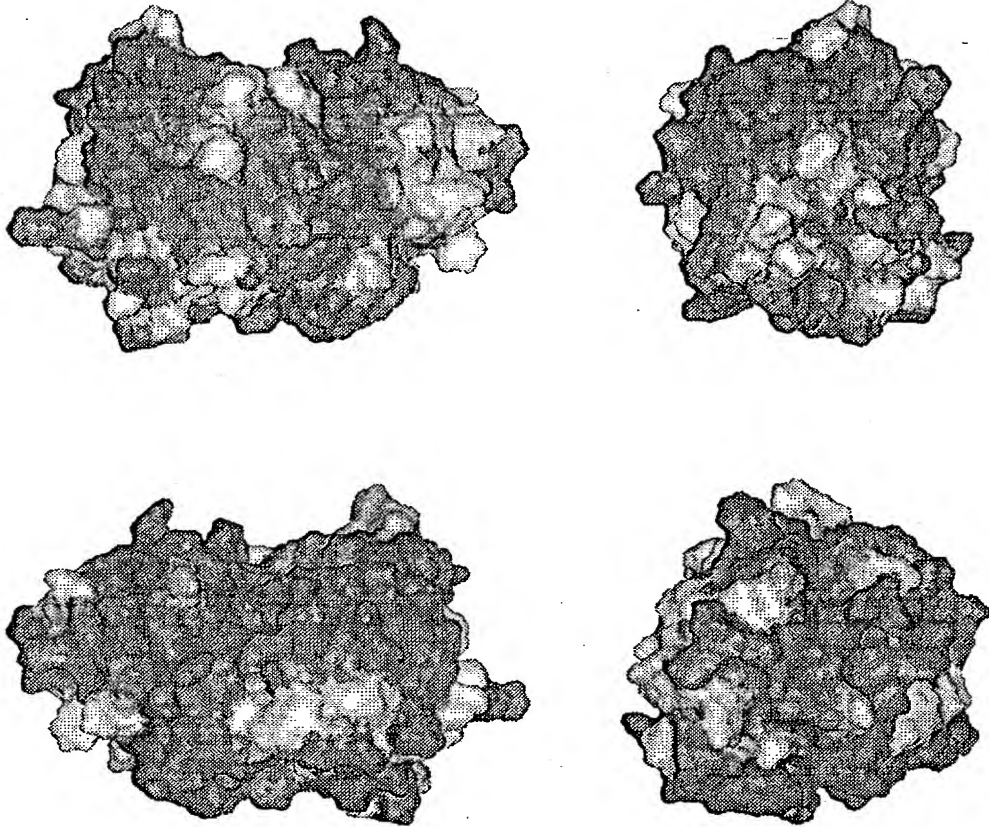
FIG. 35 B

	80	90	100	110	120	130
Derp1 ALK	I P R G I E Y I Q H N G V V Q E S Y Y R Y V A R E Q S C R R P N A Q R F G I S N Y C Q I Y P P N V N K I R E A L A Q T H					
Derp1	I P R G I E Y I Q H N G V V Q E S Y Y R Y V A R E Q S C R R P N A Q R F G I S N Y C Q I Y P P N V N K I R E A L A Q T H					
Eurm1 10101	I P R G I E Y I Q H N G V V Q E S Y Y R Y V A R E Q S C R R P N A Q R F G I S N Y C Q I Y P P N V N K I R E A L A Q T H					
Eurm1 10102	I P R G I E Y I Q H N G V V Q E S Y Y R Y V A R E Q S C R R P N A Q R F G I S N Y C Q I Y P P N V N K I R E A L A Q T H					
Derf1	I P R G I E Y I Q H N G V V Q E S Y Y R Y V A R E Q S C R R P N A Q R F G I S N Y C Q I Y P P N V N K I R E A L A Q T H					
Eurm1	I P R G I E Y I Q H N G V V Q E S Y Y R Y V A R E Q S C R R P N A Q R F G I S N Y C Q I Y P P N V N K I R E A L A Q T H					
Derf1	I P R G I E Y I Q H N G V V Q E S Y Y R Y V A R E Q S C R R P N A Q R F G I S N Y C Q I Y P P N V N K I R E A L A Q T H					
	140	150	160	170	180	190
Derp1 ALK	S A I A V I I G I K D L D A F R H Y D G R T I I Q R D N G Y Q P N Y H A V N I V G Y S N A Q G V D Y W I V R N S W D T T					
Derp1	S A I A V I I G I K D L D A F R H Y D G R T I I Q R D N G Y Q P N Y H A V N I V G Y S N A Q G V D Y W I V R N S W D T T					
Eurm1 10101	S A I A V I I G I K D L D A F R H Y D G R T I I Q R D N G Y Q P N Y H A V N I V G Y S N A Q G V D Y W I V R N S W D T T					
Eurm1 10102	T A V A V I I G I K D L N A F R H Y D G R T I I Q H D N G Y Q P N Y H A V N I V G Y G N T Q G V D Y W I V R N S W D T T					
Derf1	T A V A V I I G I K D L N A F R H Y D G R T I I Q H D N G Y Q P N Y H A V N I V G Y G N T Q G V D Y W I V R N S W D T T					
Eurm1	T A V A V I I G I K D L N A F R H Y D G R T I I Q H D N G Y Q P N Y H A V N I V G Y G N T Q G V D Y W I V R N S W D T T					
Derf1	T A V A V I I G I K D L N A F R H Y D G R T I I Q H D N G Y Q P N Y H A V N I V G Y G N T Q G V D Y W I V R N S W D T T					
	200	210	220			
Derp1 ALK	W G D N G Y G Y F A A N I D L M N I E E Y P Y V V I L					
Derp1	W G D N G Y G Y F A A N I D L M N I E E Y P Y V V I L					
Eurm1 10101	W G D N G Y G Y F A A N I D L M N I E E Y P Y V V I L					
Eurm1 10102	W G D N G Y G Y F A A N I D L M N I E E Y P Y V V I L					
Derf1	W G D S G Y G Y F A A N I L					
Eurm1	W G D S G Y G Y F A A N I L					
Derf1	W G D S G Y G Y F A A N I L					

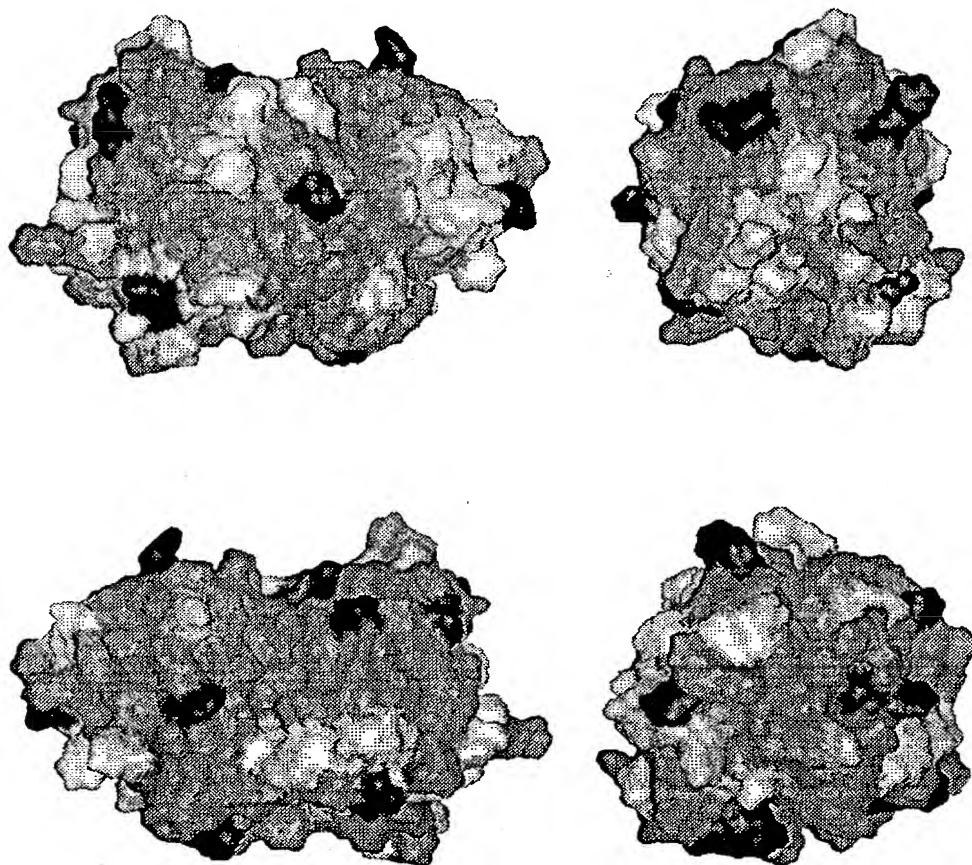
10/001,245



**FIG. 36**

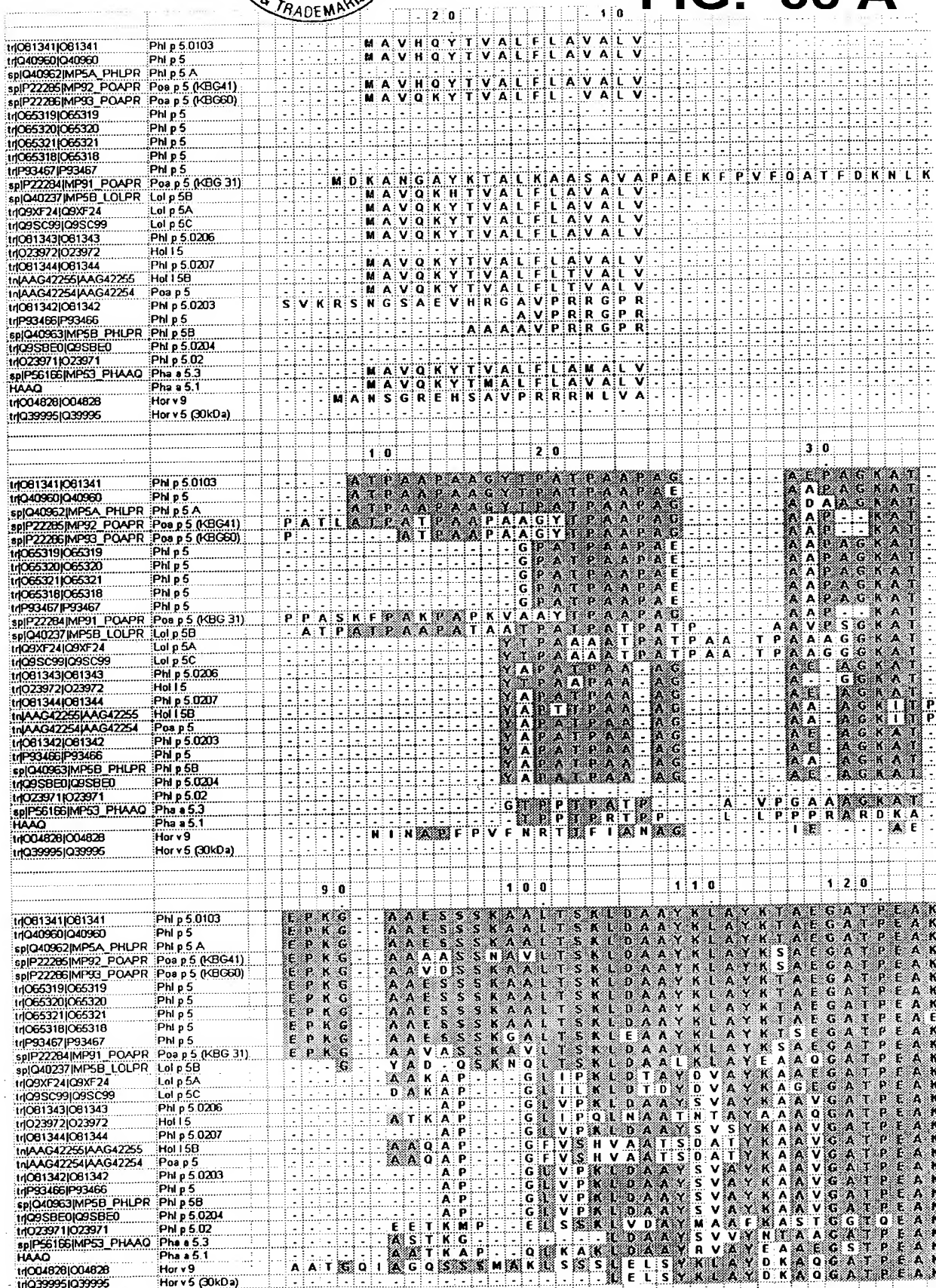


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**FIG. 37**

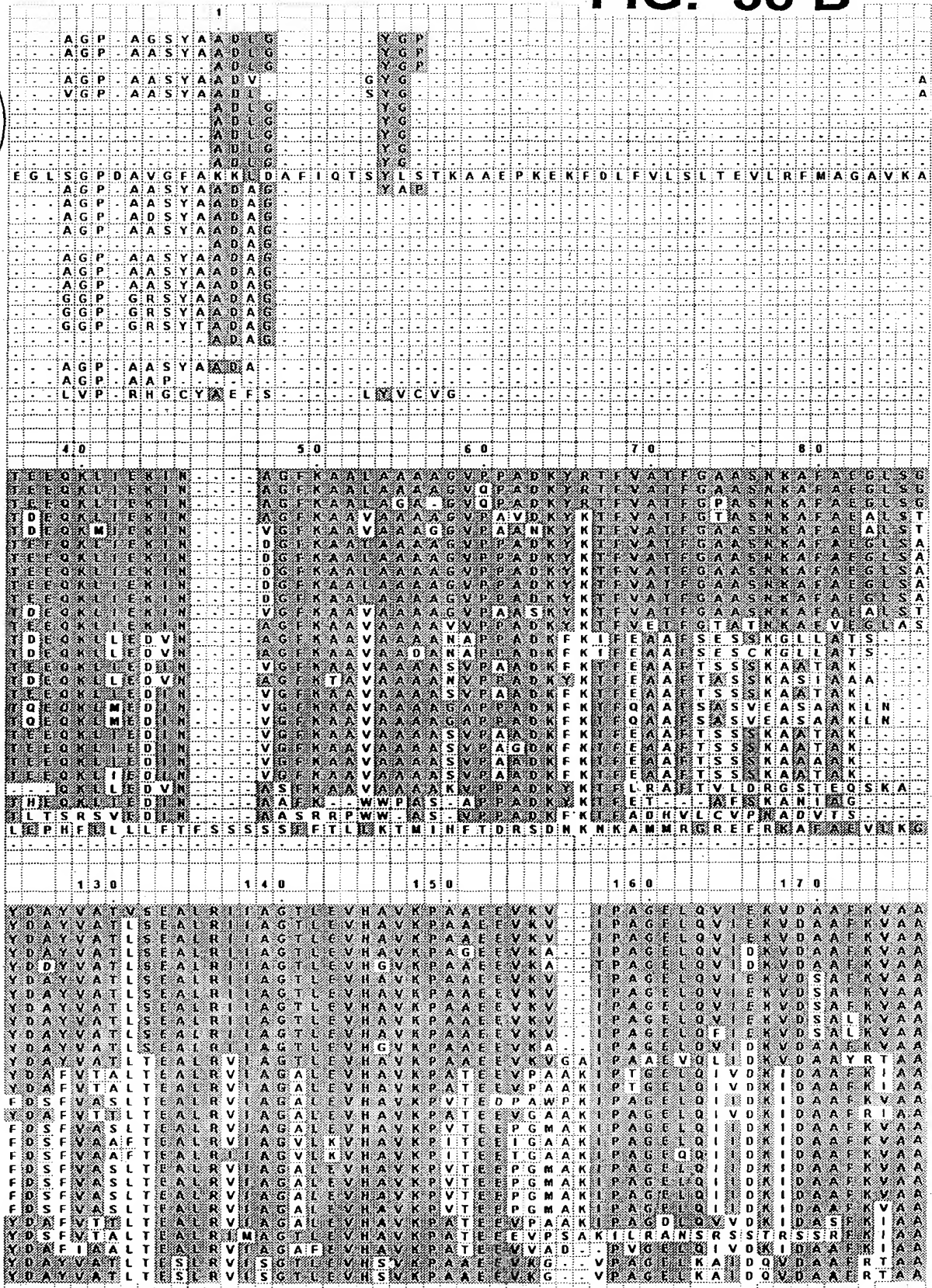


**FIG. 38 A**



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**FIG. 38 B**



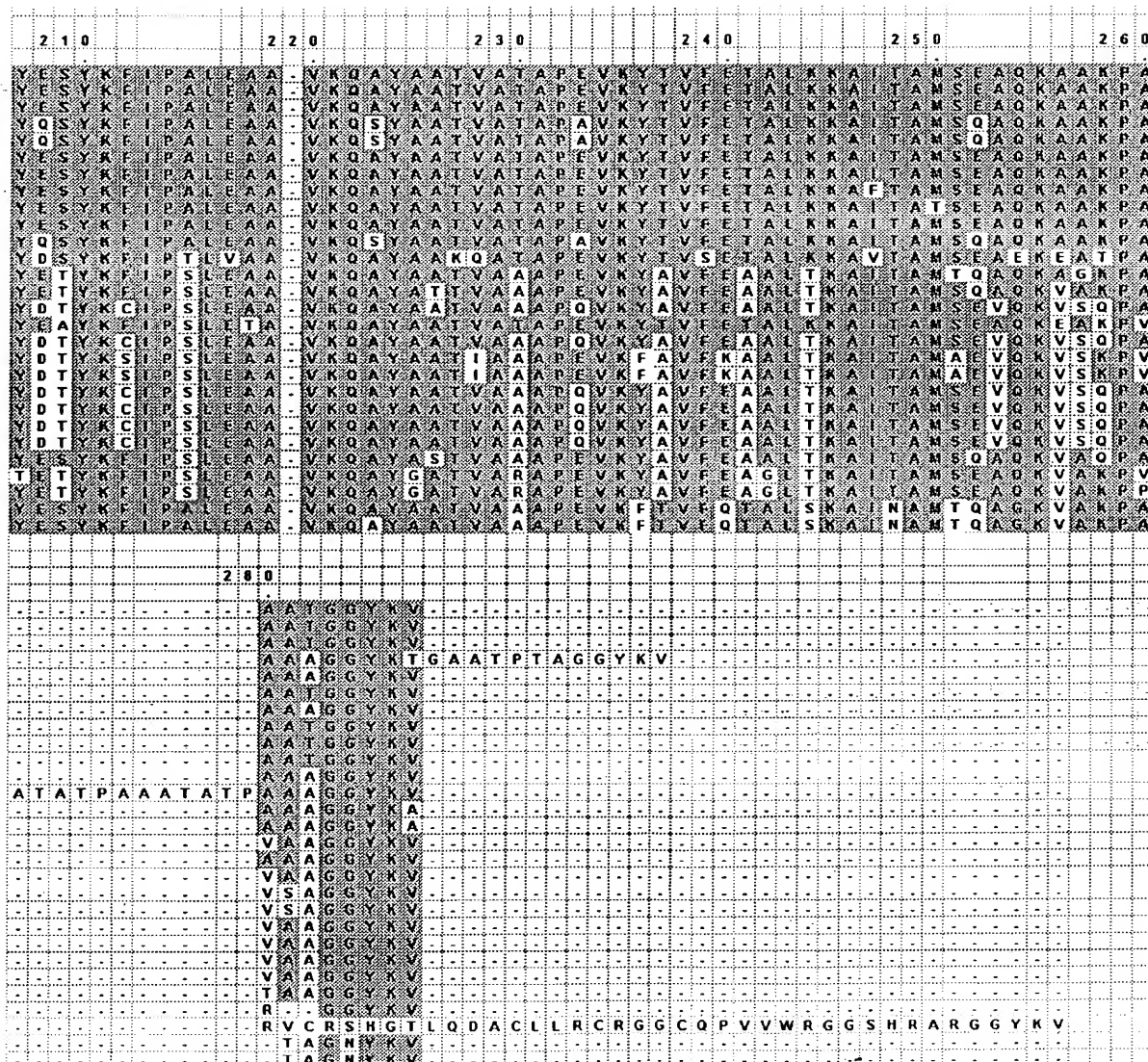


10/001,245

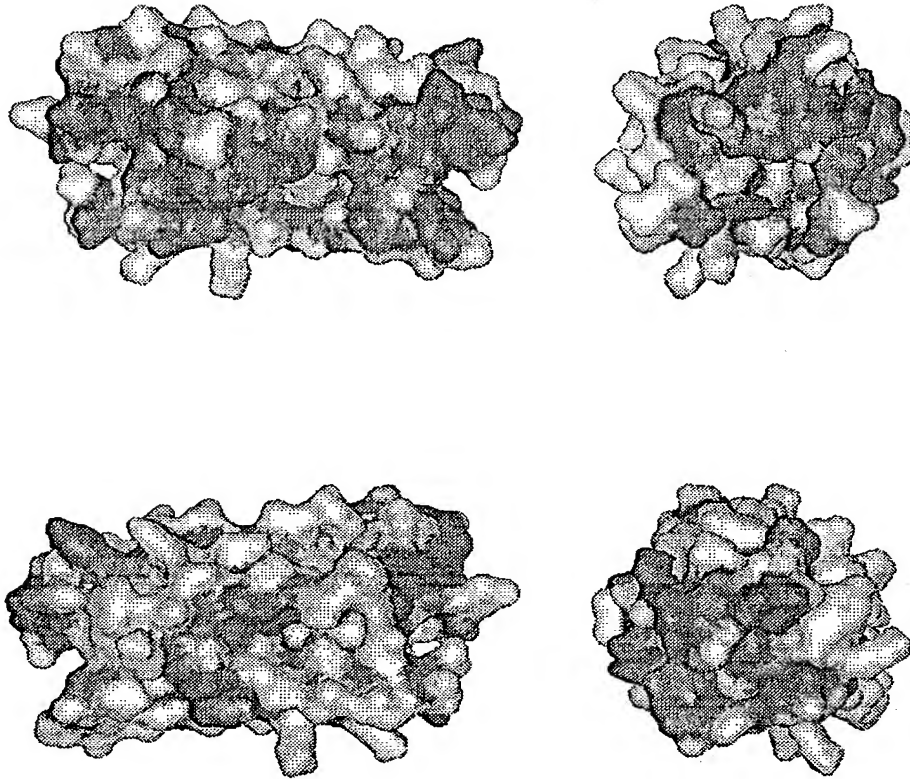


## FIG. 38 C

		1 0 0										1 9 0										2 0 0																				
tr081341 081341	Phl p 5.0103	-	-	-	-	-	-	-	-	-	-	T	A	A	H	A	A	P	A	N	D	K	F	T	V	F	E	A	A	F	N	D	A	I	K	A	S	T	G	G	A	
tr040960 040960	Phl p 5	-	-	-	-	-	-	-	-	-	-	T	A	A	N	A	A	P	A	N	D	K	F	T	V	F	E	A	A	F	N	D	E	I	K	A	S	T	G	G	A	
sp040962 MP5A_PHLPR	Phl p 5 A	-	-	-	-	-	-	-	-	-	-	T	A	A	N	A	A	P	A	N	D	K	F	T	V	F	E	A	A	F	N	D	A	I	K	A	S	T	G	G	A	
sp022265 MP92_POAPR	Poa p 5 (KBG41)	-	-	-	-	-	-	-	-	-	-	T	A	A	N	A	A	P	A	N	D	K	F	T	V	F	E	A	A	F	N	N	A	I	K	A	S	T	G	G	A	
sp022266 MP93_POAPR	Poa p 5 (KBG60)	-	-	-	-	-	-	-	-	-	-	T	A	A	N	A	A	P	A	N	D	K	F	T	V	F	E	A	A	F	N	N	A	I	K	A	S	T	G	G	A	
tr065319 065319	Phl p 5	-	-	-	-	-	-	-	-	-	-	T	A	A	N	A	A	P	A	N	D	K	F	T	V	F	E	A	A	F	N	N	A	I	K	A	S	T	G	G	A	
tr065320 065320	Phl p 5	-	-	-	-	-	-	-	-	-	-	T	A	A	N	A	A	P	A	N	D	K	F	T	V	F	E	A	A	F	N	N	A	I	K	A	S	T	G	G	A	
tr065321 065321	Phl p 5	-	-	-	-	-	-	-	-	-	-	T	A	A	N	A	A	P	A	N	D	K	F	T	V	F	E	A	A	F	N	N	A	I	K	A	S	T	G	G	A	
tr065318 065318	Phl p 5	-	-	-	-	-	-	-	-	-	-	T	A	A	N	A	A	P	A	N	D	K	F	T	V	F	E	A	A	F	N	N	A	I	K	A	S	T	G	G	A	
trP93467 P93467	Phl p 5	-	-	-	-	-	-	-	-	-	-	T	A	A	N	A	A	P	A	N	D	K	F	T	V	F	E	A	A	F	N	H	A	I	K	A	S	T	G	G	A	
sp022284 MP91_POAPR	Poa p 5 (KBG 31)	-	-	-	-	-	-	-	-	-	-	T	A	A	N	A	A	P	A	N	D	K	F	T	V	F	E	A	A	F	N	D	A	I	K	A	S	T	G	G	A	
sp040237 MP5B_LOLPR	Lol p 5B	-	-	-	-	-	-	-	-	-	-	T	A	A	N	A	A	P	A	N	D	K	F	T	V	F	E	N	T	I	N	N	A	I	K	V	S	L	G	A	A	
tr09XF24 Q9XF24	Lol p 5A	-	-	-	-	-	-	-	-	-	-	T	A	A	N	A	A	P	A	N	D	K	F	T	V	F	E	S	A	F	N	K	A	I	K	N	E	C	T	G	G	A
tr09SC99 Q9SC99	Lol p 5C	-	-	-	-	-	-	-	-	-	-	T	A	A	N	A	A	P	A	N	D	K	F	T	V	F	E	S	A	F	N	K	A	I	K	N	E	C	T	G	G	A
tr081343 081343	Phl p 5.0206	-	-	-	-	-	-	-	-	-	-	T	A	A	A	T	A	A	P	A	N	D	K	F	T	V	F	E	A	A	F	N	K	A	I	K	E	S	T	G	G	A
tr023972 023972	Hol 15	-	-	-	-	-	-	-	-	-	-	T	A	A	N	A	A	P	A	N	D	K	F	T	V	F	E	G	A	F	N	K	A	I	K	E	S	T	G	G	A	
tr081344 081344	Phl p 5.0207	-	-	-	-	-	-	-	-	-	-	T	A	A	A	T	A	A	P	A	N	D	K	F	T	V	F	E	A	A	F	N	K	A	I	K	E	S	T	G	G	A
tr081342 081342	Phl p 5.0203	-	-	-	-	-	-	-	-	-	-	T	A	A	N	A	A	P	A	N	D	K	F	T	V	F	E	A	A	F	N	N	A	I	K	E	S	T	G	G	A	
trP93466 P93466	Phl p 5	-	-	-	-	-	-	-	-	-	-	T	A	A	A	T	A	A	P	A	N	D	K	F	T	V	F	E	A	A	F	N	K	A	I	K	E	S	T	G	G	A
sp040963 MP5B_PHLPR	Phl p 5B	-	-	-	-	-	-	-	-	-	-	T	A	A	A	T	A	A	P	A	N	D	K	F	T	V	F	E	A	A	F	N	K	A	I	K	E	S	T	G	G	A
tr09SBEO Q9SBEO	Phl p 5.0204	-	-	-	-	-	-	-	-	-	-	T	A	A	A	T	A	A	P	A	N	D	K	F	T	V	F	E	A	A	F	N	K	A	I	K	E	S	T	G	G	A
tr023971 023971	Phl p 5.02	-	-	-	-	-	-	-	-	-	-	T	A	A	A	T	A	A	P	A	N	D	K	F	T	V	F	E	T	A	F	N	K	A	I	K	E	S	T	G	G	A
sp056166 MP53_PHAHQ	Pha a 5.3	T	V	A	T	P	L	S	H	S	-	T	A	A	N	S	A	P	A	N	D	K	F	T	V	F	E	G	A	F	N	K	A	I	K	E	S	T	G	G	A	
HAHQ	Pha a 5.1	-	-	-	-	-	-	-	-	-	-	T	A	A	N	S	A	P	A	N	D	K	F	T	V	F	E	G	A	F	N	K	A	I	K	E	S	T	G	G	A	
tr004828 004828	Hor v 9	-	-	-	-	-	-	-	-	-	-	T	A	A	D	A	A	P	A	N	D	K	F	T	V	F	E	S	L	Q	Q	G	P	S	R	K	P	R	G	A		
tr039995 039995	Hor v 5 (30kDa)	-	-	-	-	-	-	-	-	-	-	T	A	A	D	A	A	P	A	N	D	K	F	T	V	F	E	S	L	Q	Q	G	P	S	R	K	P	R	G	A		
		2 7 0																																								
tr081341 081341	Phl p 5.0103	A	A	-	-	-	-	-	-	-	-	A	A	T	A	T	A	T	A	A	V	G	A	A	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
tr040960 040960	Phl p 5	A	A	-	-	-	-	-	-	-	-	A	A	T	A	T	A	T	A	A	V	G	A	A	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
sp040962 MP5A_PHLPR	Phl p 5 A	A	A	-	-	-	-	-	-	-	-	A	A	T	A	T	A	T	A	A	V	G	A	A	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
sp022265 MP92_POAPR	Poa p 5 (KBG41)	A	A	-	-	-	-	-	-	-	-	V	T	A	T	A	T	G	A	V	G	A	A	T	G	A	V	G	A	A	T	-	-	-	-	-	-	-	-	-		
sp022266 MP93_POAPR	Poa p 5 (KBG60)	A	A	-	-	-	-	-	-	-	-	A	A	T	G	T	A	T	A	A	V	G	A	A	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
tr065319 065319	Phl p 5	T	E	-	-	-	-	-	-	-	-	A	A	T	A	T	A	T	A	A	V	G	A	A	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
tr065320 065320	Phl p 5	A	A	-	-	-	-	-	-	-	-	A	A	T	A	T	A	T	S	A	V	G	A	A	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
tr065321 065321	Phl p 5	T	E	-	-	-	-	-	-	-	-	A	A	T	A	T	A	T	A	A	V	G	A	A	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
tr065318 065318	Phl p 5	T	E	-	-	-	-	-	-	-	-	A	A	T	A	T	A	T	A	A	V	G	A	A	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
trP93467 P93467	Phl p 5	T	E	-	-	-	-	-	-	-	-	A	A	T	A	T	A	T	A	A	V	G	A	A	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
sp022284 MP91_POAPR	Poa p 5 (KBG 31)	A	A	-	-	-	-	-	-	-	-	V	I	G	T	A	T	S	A	V	G	A	A	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
sp040237 MP5B_LOLPR	Lol p 5B	A	A	-	-	-	-	-	-	-	-	A	A	T	P	I	P	A	A	T	A	A	T	A	T	P	A	A	A	Y	A	T	A	T	P	A	A	A	T			
tr09XF24 Q9XF24	Lol p 5A	A	A	-	-	-	-	-	-	-	-	A	A	T	G	A	T	V	A	T	C	A	A	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
tr09SC99 Q9SC99	Lol p 5C	A	A	-	-	-	-	-	-	-	-	A	A	T	G	A	T	V	A	T	C	A	A	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
tr081343 081343	Phl p 5.0206	T	G	-	-	-	-	-	-	-	-	A	A	T	V	A	A	G	A	A	T	T	A	T	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
tr023972 023972	Hol 15	A	A	-	-	-	-	-	-	-	-	A	A	T	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
tr081344 081344	Phl p 5.0207	T	G	-	-	-	-	-	-	-	-	A	A	T	V	A	A	G	A	A	T	T	A	A	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
tr081342 081342	Phl p 5.0203	T	G	-	-	-	-	-	-	-	-	A	A	T	V	A	A	G	A	A	T	T	A	A	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
trP93466 P93466	Phl p 5	T	G	-	-	-	-	-	-	-	-	A	A	T	V	A	A	G	A	A	T	T	A	A	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
sp040963 MP5B_PHLPR	Phl p 5B	T	G	-	-	-	-	-	-	-	-	A	A	T	V	A	A	G	A	A	T	T	A	A	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
tr09SBEO Q9SBEO	Phl p 5.0204	T	G	-	-	-	-	-	-	-	-	A	A	T	V	A	A	G	A	A	T	T	A	A	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
tr023971 023971	Phl p 5.02	A	A	-	-	-	-	-	-	-	-	A	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
sp056166 MP53_PHAHQ	Pha a 5.3	R	L	S	P	Q	-	-	-	-	-	P	P	Q	V	L	P	L	A	A	G	C	A	A	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
HAHQ	Pha a 5.1	L	S	P	Q	-	-	-	-	-	-																															



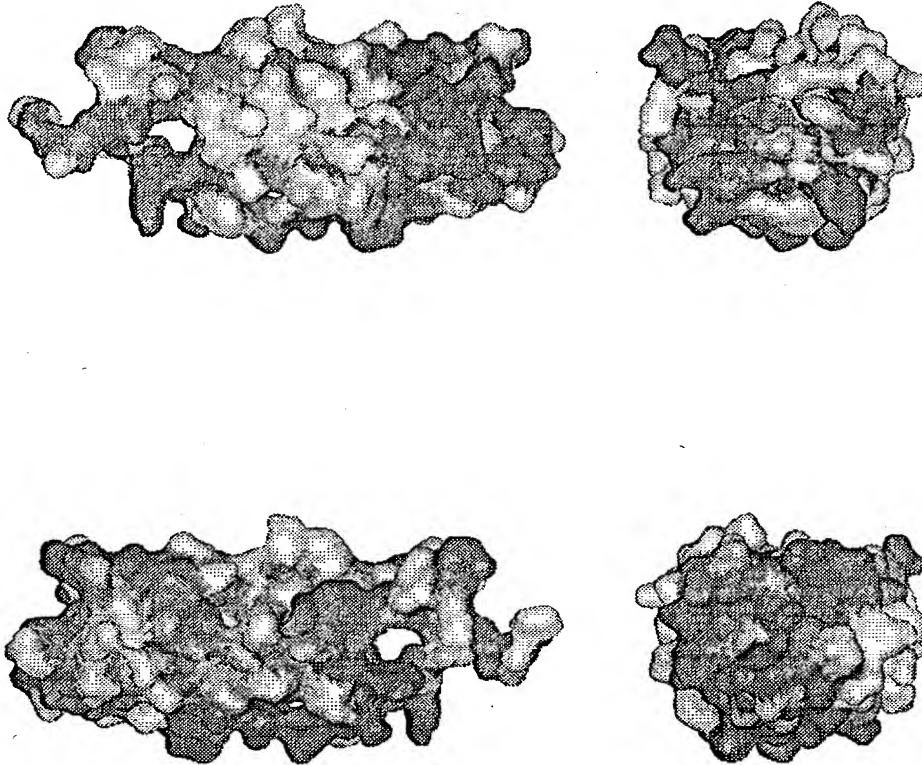
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**FIG. 39 A**

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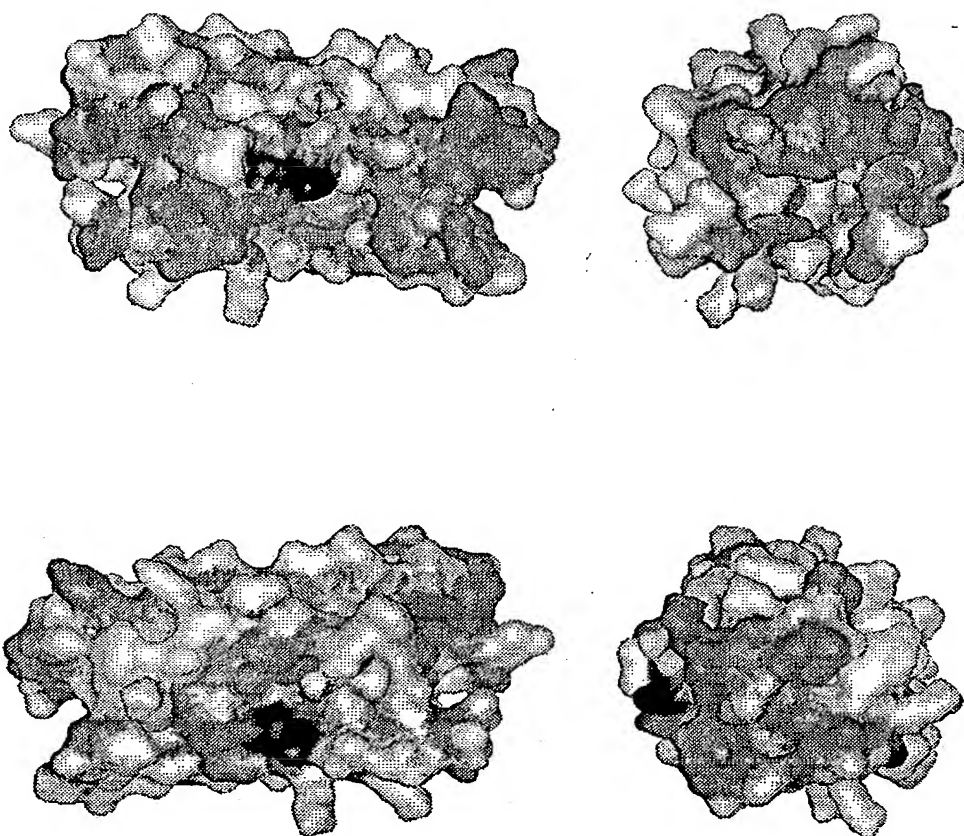
**FIG. 39 B**



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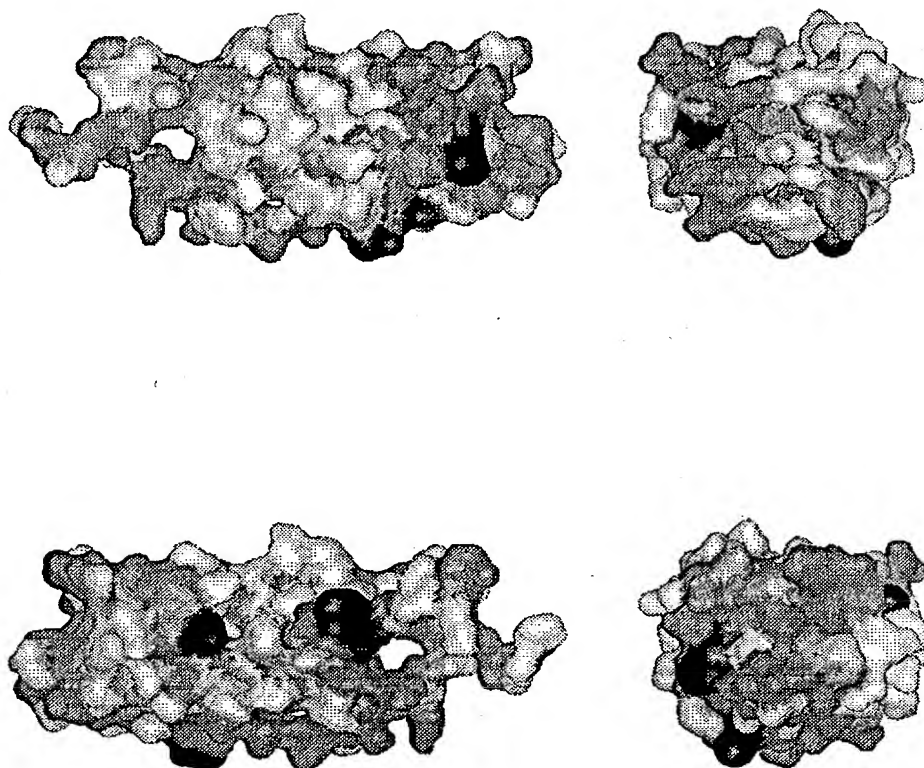
**FIG. 40 A**



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**FIG. 40 B**



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FIG. 41

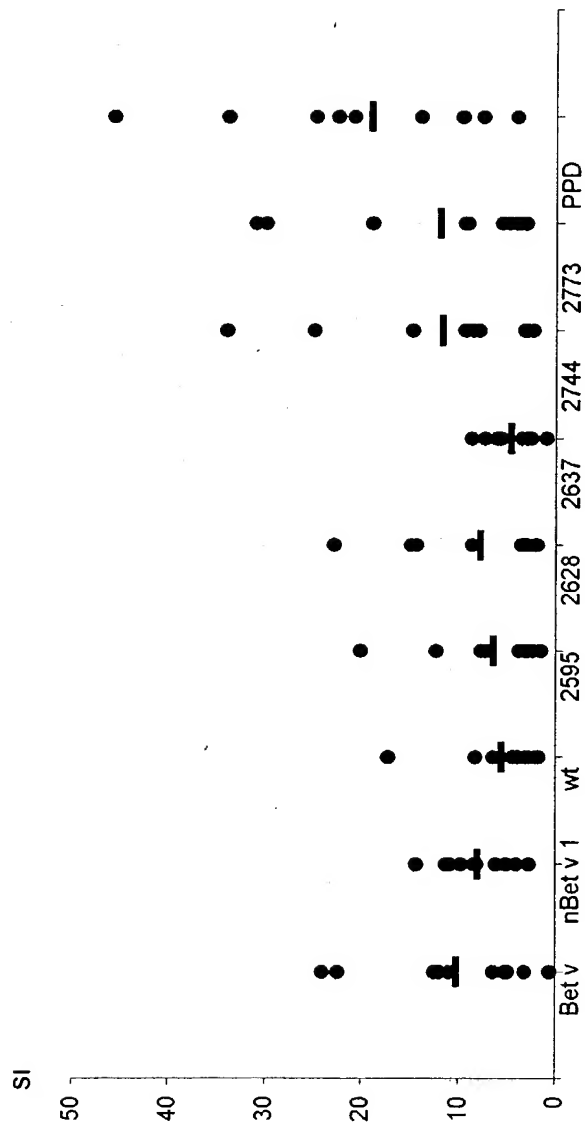
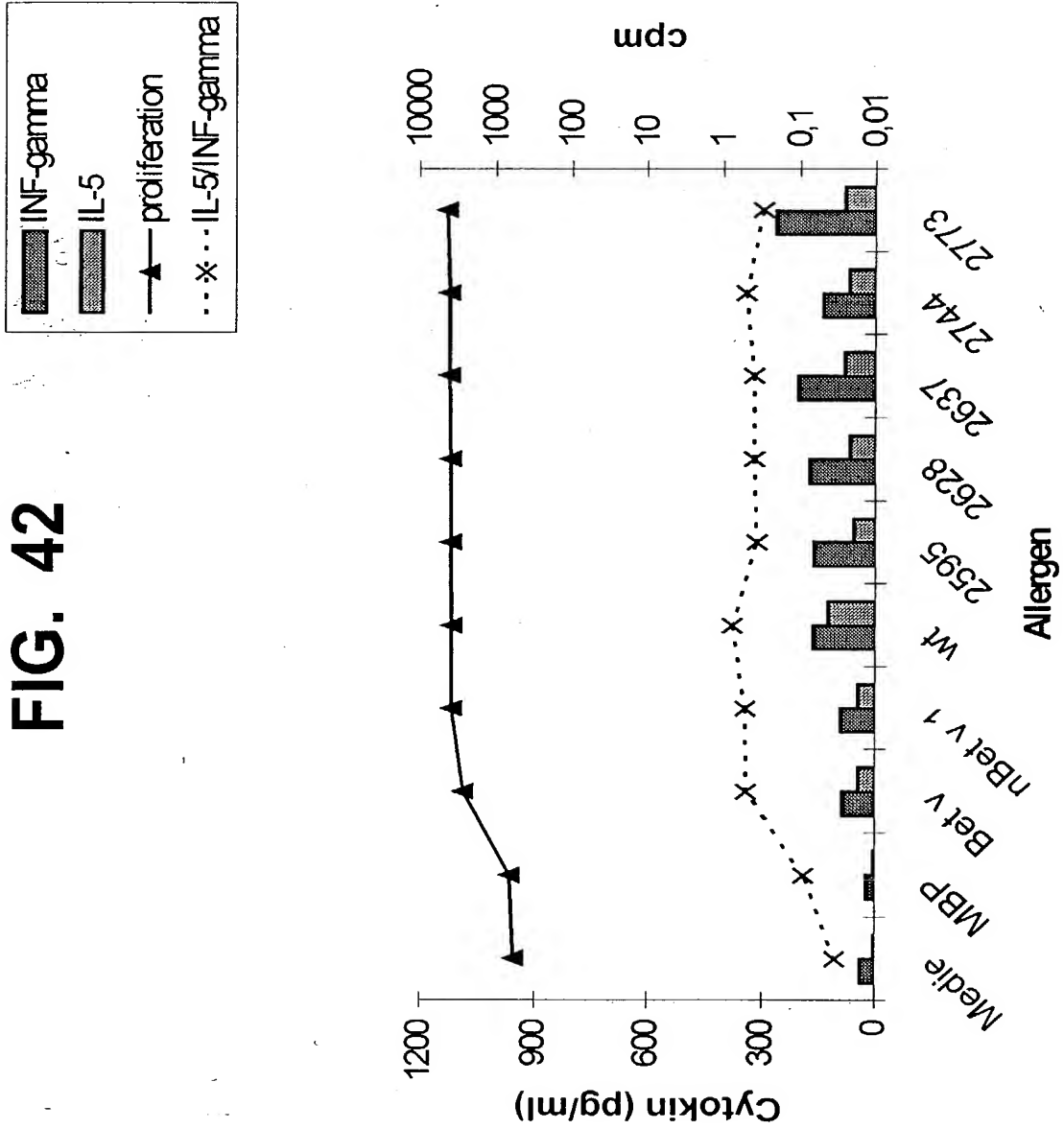




FIG. 42





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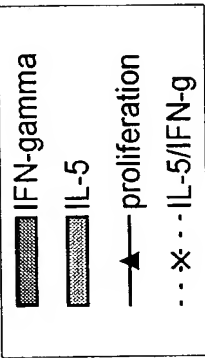


FIG. 43

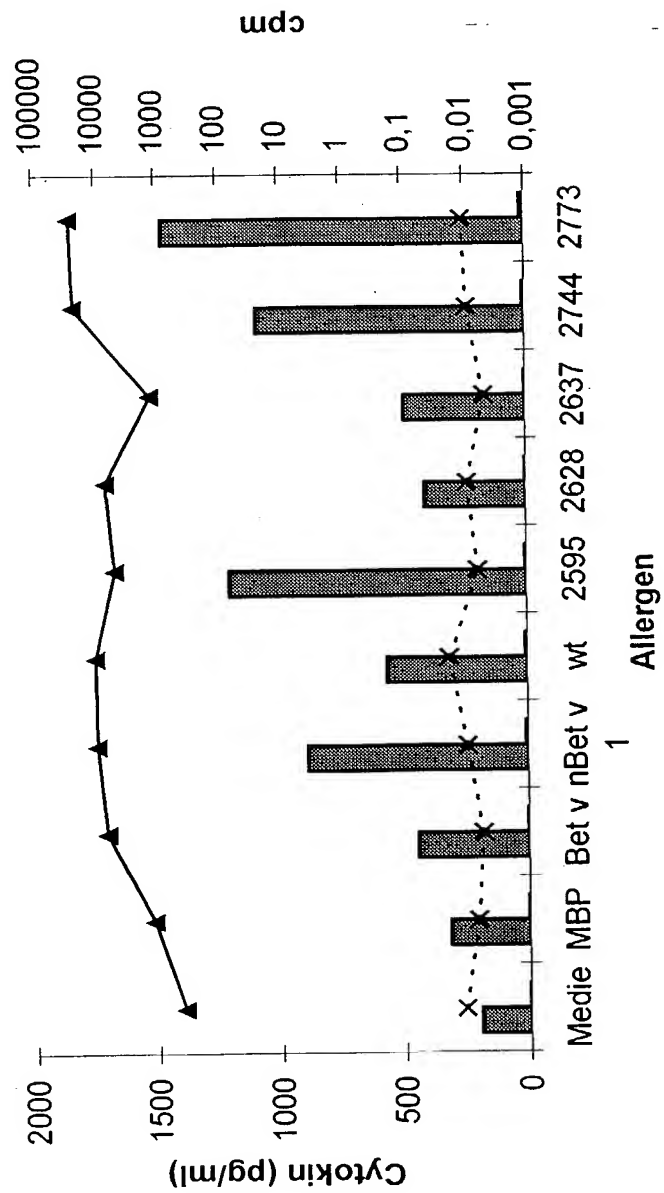




FIG. 44

